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OM protein - protein search, using sw model

Run on: April 8, 2005, 23:16:18 ; Search time 171 Seconds
(without alignments)
22.618 Million cell updates/sec

Title: US-10-058-069-17

Perfect score: 54

Sequence: 1 GGSSGGGSG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	10	6	ABR82458 Amino aci
2	54	100.0	33	6	ABR56402 Peptide 1
3	54	100.0	33	6	ABR44503 Peptide 1
4	54	100.0	41	6	ABR56404 Peptide 1
5	54	100.0	41	6	ABR44505 Peptide 1
6	54	100.0	251	8	ADS12372 Human IGF
7	54	100.0	316	8	ADQ19957 Human sof
8	54	100.0	628	8	ADS85115 Mouse ato
9	51	94.4	239	4	ABR63164 Drosophil
10	51	94.4	283	8	ADP85426 V122acFv
11	51	94.4	454	6	ABR63545 Danio rer
12	51	94.4	834	2	AAR08391 Sequence
13	50	92.6	12	5	AAR02047 T-cell sp
14	50	92.6	12	8	ADM18934 Recombina
15	50	92.6	14	2	AAR87024 Flexible
16	50	92.6	14	2	AAR23417 Linker pe
17	50	92.6	14	2	AAR47355 Polylinke
18	50	92.6	14	2	AAY17953 Amino aci
19	50	92.6	14	2	AAY23638 Linker pe
20	50	92.6	14	3	AAB03812 Polylinke
21	50	92.6	14	3	AAY99938 Peptide u
22	50	92.6	14	4	AAB62063 Sequence
23	50	92.6	14	4	AAY72751 Poly link
24	50	92.6	14	5	ABG66180 Phage dis
25	50	92.6	14	5	AAO17152 Human end

26	50	92.6	14	6	ABE70843
27	50	92.6	14	6	AAE37748
28	50	92.6	14	8	ADI47373
29	50	92.6	14	8	ADJ88260
30	50	92.6	14	8	ADM18940
31	50	92.6	14	8	ADO49278
32	50	92.6	14	8	ADQ91247
33	50	92.6	14	8	ADR01303
34	50	92.6	15	2	AAR25983
35	50	92.6	15	2	AAR59500
36	50	92.6	15	2	AAR85123
37	50	92.6	15	2	AAR76683
38	50	92.6	15	2	AAR99244
39	50	92.6	15	2	AAR95067
40	50	92.6	15	2	AAW09323
41	50	92.6	15	2	AAW49219
42	50	92.6	15	2	AAW10295
43	50	92.6	15	2	AAW35984
44	50	92.6	15	2	AAW87784
45	50	92.6	15	2	AAW43414

ALIGNMENTS

RESULT 1

ABR82458
ID ABR82458 standard; peptide; 10 AA.

AC ABR82458;

XX 20-NOV-2003 (first entry)

XX Amino acid sequence of a spacer peptide.

XX Polycistronic vector; immunosuppressive; antiinflammatory; antiallergic;
cytostatic; spacer.

XX Synthetic.

XX WO2003048306-A2.

XX 12-JUN-2003.

XX 18-NOV-2002; 2002WO-US036856.

XX 16-NOV-2001; 2001US-0331481P.

XX 05-AUG-2002; 2002US-0400687P.

XX (IDEC-) IDEC PHARM CORP.

XX Ref M, Barnett R;

XX WPI; 2003-513745/48.

XX New polycistronic expression system containing a polycistronic vector,
useful for producing or expressing functional antibodies or multiple gene
products in eukaryotic host cells.

XX Disclosure; Page 22; 132pp; English.

XX The invention relates to a polycistronic vector for expressing functional
antibodies in eukaryotic host cells. The polycistronic expression system,
i.e. polycistronic vectors and eukaryotic cells, is useful for producing
or expressing functional antibodies or multiple gene products. The
functional antibodies elicit a therapeutic effect useful for treating an
autoimmune, inflammatory, infectious, allergic or neoplastic disease. The
present sequence represents the amino acid sequence of a spacer peptide

XX Sequence 10 AA;

Query Match 100.0%; Score 54; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSSGGGSG 10
 |||||

Db 1 GSSSGGGSG 10

RESULT 2

ABR56402

ID ABR56402 standard; peptide; 33 AA.

XX AC ABR56402;

XX DT 28-JUL-2003 (first entry)

XX DE Peptide linker #2.

XX KW Antigen presenting cell; APC; immune response; virus like particle; VLP;

XX KW cytostatic; virucide; antibacterial; antiparasitic; fungicide;

XX KW antiallergic; immunosuppressive; antiaddictive; antiinflammatory;

XX KW antithyroid; antidiabetic; neuroprotective; nootropic; osteopathic;

XX KW antineumatic; antiarthritis; vaccine; immunisation; infectious disease;

XX KW anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;

XX KW graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;

XX KW Alzheimer's disease; osteoporosis; rheumatoid arthritis;

XX KW inflammatory autoimmune disease.

XX OS Synthetic.

XX WO2003024480-A2.

XX DT 27-MAR-2003.

XX PF 16-SEP-2002; 2002WO-IB004252.

XX PR 14-SEP-2001; 2001US-0318967F.

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX PI Bachmann MF, Storni T, Lechner F;

XX WPI; 2003-363095/34.

XX A composition, useful for enhancing an immune response against an antigen or a virus-like particle, enhancing anti-viral protection in an animal, or immunizing or treating tumors or infectious diseases, e.g. viral infections.

XX Disclosure; Page 64; 243pp; English.

XX The present invention describes a composition (C) for enhancing an immune response against an antigen or a virus-like particle in an animal. (C) comprises a virus-like particle (VLP) bound to at least one antigen, or a VLP capable of being recognised by the immune system of the animal. Also described: (1) enhancing an immune response against an antigen or a VLP in an animal comprising introducing (C) into the animal; (2) vaccines comprising (C) together with a pharmaceutical diluent, carrier or excipient; (3) immunising or treating an animal comprising administering the vaccine to the animal, or priming or boosting a T cell response in the animal by administering the vaccine; and (4) enhancing anti-viral protection in an animal comprising introducing (C) into the animal. (C) has cytostatic, virucide, antibacterial, antiparasitic, fungicide, antiallergic, immunosuppressive, antiaddictive, antiinflammatory, antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic, antineumatic and antiarthritic activities. (C) or the vaccines can be used for enhancing an immune response against an antigen or a VLP in an animal, enhancing anti-viral protection in an animal, or immunising or treating tumors and infectious diseases such as viral, bacterial, parasitic or fungal infections. The vaccine compositions are also useful for preventing or treating allergies, drug addiction, graft-versus-host disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis, Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509

CC represent sequences used in the exemplification of the present invention

SQ Sequence 33 AA;

Query Match 100.0%; Score 54; DB 6; Length 33;

Best Local Similarity 100.0%; Pred. No. 5;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSSGGGSG 10
 |||||

Db 15 GSSSGGGSG 24

RESULT 3

ABR44503

ID ABR44503 standard; peptide; 33 AA.

XX AC ABR44503;

XX DT 25-JUL-2003 (first entry)

XX DE Peptide linker #2.

XX KW Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;

XX KW hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;

XX KW immunostimulant; cytostatic; antiallergic; virucide; antibacterial;

XX KW immune response; immunisation; allergy; tumour; breast cancer;

XX KW neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;

XX KW chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

XX OS Synthetic.

XX WO2003024481-A2.

XX DT 27-MAR-2003.

XX PF 16-SEP-2002; 2002WO-IB004132.

XX PR 14-SEP-2001; 2001US-0318994P.

XX PR 22-APR-2002; 2002US-0374145P.

XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

XX PA (MAUR/) MAURER P.

XX PA (TISS/) TISSOT A.

XX PA (SCHW/) SCHWARZ K.

XX PA (MEIJ/) MEIJERINK E.

XX PA (LIPO/) LIPOWSKY G.

XX PA (PUMP/) PUMPENS P.

XX PA (CIEL/) CIELENS I.

XX PA (RENH/) RENHOFER R.

XX PI Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;

XX PI Pumpens P, Cielens I, Renhofs R, Bachmann MF, Storni T;

XX WPI; 2003-354564/33.

XX New compositions comprising immunostimulatory substances packaged into virus-like particles, useful as a vaccine for enhancing an immune response in animals, e.g. for treating or preventing allergies, tumors or viral infections.

XX Disclosure; Page 75; 322pp; English.

XX The present invention describes a composition (C) for enhancing an immune response in an animal. (C) comprises a virus-like particle (VLP), and an immunostimulatory substance. The immunostimulatory substance is bound to the VLP. Also described: (1) enhancing an immune response in an animal by introducing (C) into the animal; (2) producing (C) for enhancing an immune response in an animal; (3) vaccines comprising (C) together with a pharmaceutical diluent, carrier or excipient; and (4) immunising or treating an animal by: (a) administering the vaccine to the animal; (b) priming a T cell response in the animal by administering the vaccine; or (c) boosting a T cell response in the animal by administering the

CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
 CC antibacterial activities. (I) can be used in vaccines for enhancing an
 CC immune response in an animal, particularly a mammal or human.
 CC Specifically, (C) is useful for enhancing a B cell response, a T cell
 CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
 CC comprising (C) can also be used for immunising or treating an animal,
 CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
 CC reptiles or fish. (C) is particularly useful in prophylactic or
 CC therapeutic vaccines against allergies, tumours (e.g. breast cancers,
 CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
 CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
 CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 33 AA;

Query Match 100.0%; Score 54; DB 6; Length 33;
 Best Local Similarity 100.0%; Pred. No. 5;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
 |||||
 DB 15 GGSSGGGGSG 24

RESULT 4
 ABR56404
 ID ABR56404 standard; peptide; 41 AA.
 AC ABR56404;
 XX

28-JUL-2003 (first entry)
 Peptide linker #4.

Antigen presenting cell; APC; immune response; virus like particle; VLP;
 cytostatic; virucide; antibacterial; antiparasitic; fungicide;
 antiallergic; immunosuppressive; antiaddictive; antinflammatory;
 antithyroid; antidiabetic; neuroprotective; nootropic; osteopathic;
 antirheumatic; antiarthritic; vaccine; immunisation; infectious disease;
 anti-viral protection; tumour; allergy; drug addiction; Crohn's disease;
 graft-versus-host disease; Grave's disease; diabetes; multiple sclerosis;
 Alzheimer's disease; osteoporosis; rheumatoid arthritis;
 inflammatory autoimmune disease.

Synthetic.
 WO2003024480-A2.
 27-MAR-2003.

16-SEP-2002; 2002WO-IB004252.

14-SEP-2001; 2001US-0318967P.

(CYTO-) CYTOS BIOTECHNOLOGY AG.

Bachmann MF, Storni T, Lechner F;

WPI; 2003-363095/34.

A composition, useful for enhancing an immune response against an antigen
 or a virus-like particle, enhancing anti-viral protection in an animal,
 or immunizing or treating tumors or infectious diseases, e.g. viral
 infections.

Disclosure; Page 64; 243pp; English.

The present invention describes a composition (C) for enhancing an immune
 response against an antigen or a virus-like particle in an animal. (C)
 comprises a virus-like particle (VLP) bound to at least one antigen, or a
 VLP capable of being recognised by the immune system of the animal. Also
 described: (1) enhancing an immune response against an antigen or a VLP

CC in an animal comprising introducing (C) into the animal; (2) vaccines
 CC comprising (C) together with a pharmaceutical diluent, carrier or
 CC excipient; (3) immunising or treating an animal comprising administering
 CC the vaccine to the animal, or priming or boosting a T cell response in
 CC the animal by administering the vaccine; and (4) enhancing anti-viral
 CC protection in an animal comprising introducing (C) into the animal. (C)
 CC has cytostatic, virucide, antibacterial, antiparasitic, fungicide,
 CC antiallergic, immunosuppressive, antiaddictive, antinflammatory,
 CC antithyroid, antidiabetic, neuroprotective, nootropic, osteopathic,
 CC antirheumatic and antiarthritic activities. (C) or the vaccines can be
 CC used for enhancing an immune response against an antigen or a VLP in an
 CC animal, enhancing anti-viral protection in an animal, or immunising or
 CC treating tumours and infectious diseases such as viral, bacterial,
 CC parasitic or fungal infections. The vaccine compositions are also useful
 CC for preventing or treating allergies, drug addiction, graft-versus-host
 CC disease, Crohn's disease, Grave's disease, diabetes, multiple sclerosis,
 CC Alzheimer's disease, osteoporosis, rheumatoid arthritis, or inflammatory
 CC autoimmune disease. ACC69838 to ACC69852 and ABR56401 to ABR56509
 CC represent sequences used in the exemplification of the present invention
 XX
 SQ Sequence 41 AA;

Query Match 100.0%; Score 54; DB 6; Length 41;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
 |||||
 DB 9 GGSSGGGGSG 18

RESULT 5
 ABR44505
 ID ABR44505 standard; peptide; 41 AA.
 XX ABR44505;

25-JUL-2003 (first entry)

Peptide linker #4.

Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV;
 hepatitis B virus; lymphocytic choriomeningitis virus; vaccine;
 immunostimulant; cytostatic; antiallergic; virucide; antibacterial;
 immune response; immunisation; allergy; tumour; breast cancer;
 neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
 chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.

Synthetic.

WO2003024481-A2.

27-MAR-2003.

16-SEP-2002; 2002WO-IB004132.

14-SEP-2001; 2001US-0318994P.

22-APR-2002; 2002US-0374145P.

(CYTO-) CYTOS BIOTECHNOLOGY AG.

(MAUR-) MAURER P.

(TISS-) TISSOT A.

(SCHW-) SCHWARZ K.

(MEIJ-) MEIJERINK E.

(LIPO-) LIPOWSKY G.

(PUMP-) PUMPS P.

(CIEL-) CIELENS I.

(RENH-) RENHOFA R.

Maurer P, Tissot A, Schwarz K, Meijerink E, Lipowsky G;

Pumps P, Cielens I, Renhofa R, Bachmann MF, Storni T;

WPI; 2003-354564/33.

XX New compositions comprising immunostimulatory substances packaged into
PT virus-like particles, useful as a vaccine for enhancing an immune
PT response in animals, e.g. for treating or preventing allergies, tumors or
XX viral infections.
XX
XX Disclosure; Page 75; 322pp; English.
XX
XX The present invention describes a composition (C) for enhancing an immune
CC response in an animal. (C) comprises a virus-like particle (VLP), and an
CC immunostimulatory substance. The immunostimulatory substance is bound to
CC the VLP. Also described: (1) enhancing an immune response in an animal by
CC introducing (C) into the animal; (2) producing (C) for enhancing an
CC immune response in an animal; (3) vaccines comprising (C) together with a
CC pharmaceutical diluent, carrier or excipient; and (4) immunising or
CC treating an animal by: (a) administering the vaccine to the animal; (b)
CC priming a T cell response in the animal by administering the vaccine; or
CC (c) boosting a T cell response in the animal by administering the
CC vaccine. (C) has immunostimulant, cytostatic, antiallergic, virucide and
CC antibacterial activities. (1) can be used in vaccines for enhancing an
CC immune response in an animal, particularly a mammal or human.
CC Specifically, (C) is useful for enhancing a B cell response, a T cell
CC response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine
CC comprising (C) can also be used for immunising or treating an animal,
CC e.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds,
CC reptiles or fish. (C) is particularly useful in prophylactic or
CC therapeutic vaccines against allergies, tumours (e.g. breast cancers,
CC neuroblastoma, or leukaemia), viral diseases (e.g. influenza, hepatitis,
CC measles or chicken pox), or bacterial infections (e.g. tuberculosis,
CC pneumonia or syphilis). ACC69790 to ACC69815 and ABR44502 to ABR44612
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 41 AA;
SQ

Query Match 100.0%; Score 54; DB 6; Length 41;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
Db 9 GGSSGGGGSG 18
|||||
|||||

RESULT 6
ADS12372
ID ADS12372 standard; protein; 251 AA.
XX
XX ADS12372;
XX
XX 16-DEC-2004 (first entry)
XX
XX Human IGF-IR antibody identified as PINT-7A4 Seq 3.
XX
XX human; antibody; insulin-like growth factor I receptor; IGF-IR;
KW somatomedin-C; cancer; inflammation; pathological liver condition;
KW cytostatic; antiinflammatory; hepatotropic; gene therapy.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO2004083248-A1.
XX
XX 30-SEP-2004.
XX
XX 04-MAR-2004; 2004WO-1B000646.
XX
XX 14-MAR-2003; 2003US-0455094P.
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Morton PA, Arbuckle JA, Bailey KJ, Nicastro PJ, Runnels HA;
PI WPI; 2004-691024/67.
XX
XX

DR N-PSDB; ADS12391.
XX
XX New antibody that specifically binds to insulin-like growth factor I
PT receptor for diagnosing or treating cancer, inflammation or pathological
PT liver conditions.
XX
XX Claim 1; SEQ ID NO 3; 258pp; English.
XX
XX This invention relates to a novel antibody or its antigen binding portion
CC that binds to the insulin-like growth factor I receptor (IGF-IR), also
CC known as somatomedin-C, in order to inhibit binding of IGF-I and IGF-II
CC to the receptor (IGF-IR). Specifically, it refers to an IGF-IR antibody
CC selected from PINT-6A1, PINT-7A2, PINT-7A4, PINT-7A5, PINT-7A6, PINT-8A1,
CC PINT-9A2, PINT-11A1, PINT-11A2, PINT-11A3, PINT-11A4, PINT-11A5, PINT-
CC 11A7, PINT-11A12, PINT-12A1, PINT-12A2, PINT-12A3, PINT-12A4, and PINT-
CC 12A5 or fragments derived thereof. The present invention describes an
CC isolated cell line (and non-human transgenic animals) useful for
CC expressing nucleic acid molecules that encode at least one variable light
CC (VL) and at least one variable heavy (VH) chain antibody regions, as well
CC as the pharmaceutical compositions derived thereof. Accordingly, it
CC provides a method of diagnosing the presence or location of an IGF-IR-
CC expressing tissue, a method for treating diseases such as cancer, as well
CC as diagnosing or treating inflammation and other pathological liver
CC conditions. As such, these compositions exhibit cytostatic,
CC antiinflammatory and hepatotropic activities and can be used for gene
CC therapy purposes. This polypeptide sequence is a human IGF-IR antibody
CC (scrFv) protein of the invention.
XX
XX Sequence 251 AA;
SQ

Query Match 100.0%; Score 54; DB 8; Length 251;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
Db 130 GGSSGGGGSG 139
|||||
|||||

RESULT 7
ADQ19957
ID ADQ19957 standard; protein; 316 AA.
XX
XX ADQ19957;
XX
XX 26-AUG-2004 (first entry)
XX
XX Human soft tissue sarcoma-upregulated protein - SEQ ID 2777.
XX
XX soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
XX Homo sapiens.
XX
XX WO2004048938-A2.
XX
XX 10-JUN-2004.
XX
XX 26-NOV-2003; 2003WO-US038193.
XX
XX 26-NOV-2002; 2002US-0429739P.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Aziz N, Ginsburg WM, Zlotnik A;
PI WPI; 2004-441208/41.
XX
XX Early detection of soft tissue sarcoma comprises determining expression
PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
XX Example 2; SEQ ID NO 2777; 210pp; English.
PS

XX The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the
 CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 XX

SQ Sequence 316 AA;

Query Match 100.0%; Score 54; DB 8; Length 316;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
 |||||
 DB 231 GGSSGGGGSG 240

RESULT 8

ADS85115
 ID ADS85115 standard; protein; 628 AA.

XX

AC ADS85115;

XX

DT 18-NOV-2004 (first entry)

XX

DE Mouse atopic dermatitis-related protein sequence SeqID117.

XX

KW atopic dermatitis; gene expression level; skin; inflammation; rash;
 KW dermatological; antiinflammatory; antipsoriatic; psoriasis; mouse;
 KW murine.

XX

OS Mus musculus.

XX

PN WO2004031386-A1.

XX

PD 15-APR-2004.

XX

PF 01-AUG-2003; 2003WO-JP009808.

XX

PR 06-AUG-2002; 2002JP-00229318.

XX

PR 14-MAY-2003; 2003JP-00136543.

XX

PA (GENO-) GENOX RES INC.

XX

PA (UYJU-) UNIV JUNTENDO.

XX

PI Itoh M, Ogawa K, Shinagawa A, Sudo H, Ogawa H, Ra C;
 PI Mitsuishi K;

XX

DR WPI; 2004-330185/30.

XX

DR N-PSDB; ADS85114.

XX

PT Determination of difference in expression level of specified genes in
 PT inflamed and non-inflamed skin sites for diagnosis and examination of
 PT atopic dermatitis and psoriasis.

XX

PS Example 1; SEQ ID NO 117; 611pp; Japanese.

XX

CC This invention relates to a novel method for the examination of atopic
 CC dermatitis in which the expression level of specified genes in specimens
 CC of skin taken from inflamed (rash) areas and non-inflamed areas is
 CC compared and the presence of increased or reduced expression in the
 CC inflamed areas determined. The invention may be useful for the
 CC development of compounds with a dermatological, antiinflammatory or
 CC antipsoriatic activity acting as inhibitors and stimulators of genes

CC involved in atopic dermatitis and psoriasis. The invention may be useful
 CC for treatment, prevention, diagnosis and assessment of atopic dermatitis
 CC and psoriasis. The present sequence is that of an atopic dermatitis-
 CC related protein which was used in the exemplification of the invention.

SQ Sequence 628 AA;

Query Match 100.0%; Score 54; DB 8; Length 628;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
 |||||
 DB 551 GGSSGGGGSG 560

RESULT 9

ABB63164

ID ABB63164 standard; protein; 239 AA.

XX

AC ABB63164;

XX

DT 26-MAR-2002 (first entry)

XX

DE Drosophila melanogaster polypeptide SEQ ID NO 16284.

XX

KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

XX

OS Drosophila melanogaster.

XX

PN WO200171042-A2.

XX

PD 27-SEP-2001.

XX

PF 23-MAR-2001; 2001WO-US009231.

XX

PR 23-MAR-2000; 2000US-0191637P.

XX

PR 11-JUL-2000; 2000US-00614150.

XX

PA (PEKE) PE CORP NY.

XX

PI Venter JC, Adams M, Li PWD, Myers EW;

XX

DR WPI; 2001-656860/75.

XX

DR N-PSDB; ABL07267.

XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.

XX

PS Disclosure; SEQ ID NO 16284; 21pp + Sequence Listing; English.

XX

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 239 AA;

Query Match 94.4%; Score 51; DB 4; Length 239;
 Best Local Similarity 90.0%; Pred. No. 68;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
 |||||

DB 98 GGSSGGGGAG 107

RESULT 10

ADP85426
ID ADF85426 standard; protein; 283 AA.

XX AC ADF85426;
DT 26-FEB-2004 (first entry)
XX DE V12scFv clone.

XX KW Fv library.

XX OS Unidentified.

XX PN JP2003334075-A.

XX PD 25-NOV-2003.

XX PF 21-MAY-2002; 2002JP-00145858.

XX PR 21-MAY-2002; 2002JP-00145858.

XX PA (NIBS) JAPAN TOBACCO INC.

XX DR WPI; 2004-027982/03.

XX DR N-PSDB; ADF85425.

PT Mutated Fv library useful for screening mutated Fv for preparation of
PT mutated antibody for diagnostic purposes, having mutations at specific
PT amino acid positions of complementarity determining regions of antibody.

XX PS Disclosure; SEQ ID NO 2; 17pp; Japanese.

XX CC The present invention relates to mutated Fv library having mutations
CC designed such that the amino acid at position k (k is integer 2≤k≤
CC 20) is introduced at amino acid position m (m is integer 2≤m≤(n-1))
CC chosen from a region consisting of n residues (n is integer 3≤n
CC contained in complementarity determining regions (CDR) or other closer
CC regions of an antibody, and forms limited Fv repertory of (n) C m ×
CC ;km. The invention can be used for efficiently acquiring mutated
CC antibody. The present sequence represents V12scFv clone.

XX SQ Sequence 283 AA;

Query Match 94.4%; Score 51; DB 8; Length 283;
Best Local Similarity 90.0%; Pred. No. 79;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
DB 138 GGASGGGGSG 147

RESULT 11

ABR63545
ID ABR63545 standard; protein; 464 AA.

XX AC ABR63545;

XX DT 18-SEP-2003 (first entry)

XX DE Danio rerio foxd3 homologue murine HFH2.

XX KW Craniofacial malformation; variant foxd3; osteopathic; cardiant;
XX cytotstatic; auditory; neuroprotective; cleft palate syndrome;
XX congenital heart disease; cancer; mouse; HFH2.

XX OS Mus musculus.

XX PN WO2003048196-A2.

XX XX

PD 12-JUN-2003.

XX PF 09-DEC-2002; 2002WO-EP013936.

XX PR 07-DEC-2001; 2001EP-00129205.

XX PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEI.

XX PI Knapik E, Sachdev S;

XX DR WPI; 2003-513737/48.

XX PT New foxd3 polynucleotide and their (ant)agonists, useful for diagnosing
XX and treating craniofacial malformations, such as cleft palate syndrome,
XX loss of middle ear ossicles, congenital heart disease, cancer and mental
XX retardation.

XX PS Claim 34; Page 66-67; 70pp; English.

XX CC The present invention provides the protein and coding sequences of Danio
XX rerio foxd3. These can be used in the diagnosis and treatment of
XX craniofacial malformations, such as cleft palate syndrome, loss of middle
XX ear ossicles, congenital heart disease, Niikawa-Kuroki syndrome, cancer
XX and mental retardation. The present sequence is a homologue of the
XX zebrafish foxd3 protein, and is murine HFH2

XX SQ Sequence 464 AA;

Query Match 94.4%; Score 51; DB 6; Length 464;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
DB 375 GGSAGGGGSG 384

RESULT 12

AAR08391
ID AAR08391 standard; protein; 834 AA.

XX AC AAR08391;

XX DT 25-FEB-1991 (first entry)

XX DE Sequence encoded by vector pTλ for human RF-X.

XX KW MHC class II; down regulation; autoimmune disease.

XX OS Homo sapiens.

XX PN WO9012812-A.

XX PD 01-NOV-1990.

XX PF 18-APR-1989; 89EP-00106944.

XX PR 18-APR-1989; 89EP-00106944.

XX PR 14-AUG-1989; 89EP-00115008.

XX PA (MACH/) MACH B.

XX PI Mach B;

XX DR WPI; 1990-348429/46.

XX DR N-PSDB; AAQ07000.

XX PT Purified proteins and compens. - regulate expressions of MHC class II
XX genes, and bind to controlling DNA sequences.

XX PS Disclosure; Fig 6; 83pp; English.

XX CC The sequence encodes a protein which regulates the expression of MHC

CC class II genes by binding to DNA sequences which control this expression.
 CC The protein causes down-regulation, useful for the prevention and
 CC treatment of autoimmune diseases such as Insulin Dependent diabetes,
 CC Multiple Sclerosis, Lupus Erythematosus and Rheumatoid Arthritis. The
 CC protein can also be used for screening and identifying substances capable
 CC of inhibiting the expression of the MHC II genes. See also AAR08338,
 CC AAR07661, and AAR08390
 XX

SQ Sequence 834 AA;

Query Match 94.4%; Score 51; DB 2; Length 834;
 Best Local Similarity 90.0%; Pred. No. 2.1e+02;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
 |||:|||||
 Db 255 GGSTGGGGSG 264

RESULT 13

ADM18934
 ID AAR082047 standard; peptide; 12 AA.

XX

AC AAR082047;

XX

DT 09-APR-2002 (first entry)

XX

DE T-cell specific binding ligand peptide construct peptide spacer #2.

XX T-cell binding ligand; TCBL; peptide G'; human MHC class II beta chain;
 KW peptide J; human beta-2-microglobulin; HIV-1; TCBL peptide construct;
 KW immunological disorder; immune response; human immunodeficiency virus;
 KW herpes simplex virus infection; HSV; malaria; tuberculosis; cancer; CEA;
 KW acquired immunodeficiency syndrome; AIDS; allergy; autoimmune disease;
 KW autoimmune myocarditis; cytostatic; antiinflammatory.

XX Synthetic.

XX WO200189286-A2.

PN

XX

XX

PD 29-NOV-2001.

XX

XX 24-MAY-2001; 2001WO-US016793.

XX

XX 24-MAY-2000; 2000US-0206548P.

XX

PA (CELS-) CEL-SCI CORP.

XX

PI Zimmerman DS, Sarin PS;

XX

DR WPI; 2002-083037/11.

XX

XX New T cell binding ligand peptide for treating immunological disorders

PT such as herpes simplex virus, tuberculosis, cancers, acquired

PT immunodeficiency syndrome and allergies.

XX

PS Disclosure; Page 18; 110pp; English.

XX

CC The present invention relates to novel T-cell binding ligand (TCBL)
 CC peptides (e.g. peptide G' (modified human MHC class II beta chain peptide
 CC G, peptide J (human beta-2-microglobulin peptide) and HIV-1 peptides) and
 CC TCBL peptide constructs for treating immunological disorders. The peptide
 CC constructs are useful for eliciting a cellular immune response in a human
 CC patient. The method comprises administering the peptide construct to the
 CC patient preferably in combination with an immune response adjuvant. The
 CC peptide constructs in the form of conjugated peptides are useful for
 CC eliciting a cellular immune response in a patient exposed to or at risk
 CC for exposure to the human immunodeficiency virus (HIV). The TCBL peptides
 CC are useful for treating a patient suffering from an immunological
 CC disorder such as herpes simplex virus (HSV) infection, malaria,
 CC tuberculosis, cancers, acquired immunodeficiency syndrome (AIDS),
 CC allergies, autoimmune diseases (e.g. arthritis, Graves disease, multiple
 CC sclerosis (MS), autoimmune myocarditis, diabetes and lupus) by

CC administering a peptide construct comprising a TCBL peptide bonded to an
 CC antigenic peptide associated with the disorder. Unlike prior art peptide
 CC conjugates, a modified version of peptide G has long range stabilisation
 CC and also enhances the immune response. AAR082019-AAR082114 represent T-cell
 CC specific binding ligand peptides, peptide constructs or peptides used in
 CC their construction
 XX

SQ Sequence 12 AA;

Query Match 92.6%; Score 50; DB 5; Length 12;
 Best Local Similarity 90.0%; Pred. No. 6.1;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
 |||:|||||
 Db 2 GGSSGGGGSG 11

RESULT 14

ADM18934

ID ADM18934 standard; peptide; 12 AA.

XX

AC ADM18934;

XX

DT 01-JUL-2004 (first entry)

XX

DE Recombinant Tn3 resolvase linker peptide #6.

XX gene therapy; serine recombinase; catalytic domain; DNA binding domain;

KW Tn3 resolvase; transgenic application.

XX Synthetic.

PN WO2004029233-A2.

XX

PD 08-APR-2004.

XX

PF 25-SEP-2003; 2003WO-GB004169.

XX

PR 25-SEP-2002; 2002GB-00022229.

XX

PA (UNIU) UNIV GLASGOW.

XX

PI Stark WM, Akopian A;

XX

DR WPI; 2004-316113/29.

XX

PS Claim 36; Page 76; 95pp; English.

XX

CC The invention relates to a serine recombinase comprising a catalytic
 CC domain and a DNA binding domain, where the catalytic domain is mutated at
 CC G101 or at a position corresponding to G101 of Tn3 resolvase. The methods
 CC and compositions of the present invention are useful in biotechnology,
 CC gene therapy or transgenic applications. This sequence corresponds to a
 CC linker sequence used in the invention.

SQ Sequence 12 AA;

Query Match 92.6%; Score 50; DB 8; Length 12;
 Best Local Similarity 90.0%; Pred. No. 6.1;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
 |||:|||||
 Db 1 GGSSGGGGSG 10

RESULT 15

AAR87024

ID AAR87024 standard; peptide; 14 AA.
 XX AC AAR87024;
 XX DT 11-JUN-1996 (first entry)
 XX DE Flexible linker sequence.
 XX KW BZLF2; Epstein-Barr virus; EBV; C-type lectin; beta chain; MHC; antigen;
 KW major histocompatibility complex; immunoglobulin; cytotoxic T cell;
 KW autoimmune disease; myasthenia gravis; multiple sclerosis; allergy;
 KW systemic lupus erythematosus; organ transplant rejection; asthma; IL-7;
 KW tissue transplant rejection; therapy; cancer; viral disease; mouse;
 KW interleukin-7.
 XX OS Synthetic.
 XX PN W09530015-A2.
 XX PD 09-NOV-1995.
 XX PF 28-APR-1995; 95WO-US005348.
 XX PR 28-APR-1994; 94US-00235397.
 XX PA (IMV) IMMUNEX CORP.
 XX PA (UMOR) UNIV MISSOURI.
 XX PA (USSH) US NAT INST OF HEALTH.
 XX PI Alderson M, Armitage RJ, Cohen JI, Comeau MR, Farrah TM;
 XX PI Hutt-Fletcher LM, Spriggs MK;
 XX DR WPI; 1995-393086/50.
 XX PT Epstein-Barr virus BZLF2 fusion proteins - used for treating e.g. auto-
 XX PT immune disease, transplant rejection, allergy, asthma, cancer or viral
 XX PT infection.
 XX PS Example 1; Page 39; 5lpp; English.
 XX CC This sequence represents a flexible linker sequence, and was used in
 CC creating a BZLF2-immunoglobulin Fc fusion protein (BZLF2/Fc). BZLF2 is a
 CC Epstein-Barr virus (EBV) protein. To create BZLF2/Fc, this sequence, the
 CC leader sequence of mouse interleukin-7 (IL-7) (see AAR87021), a flag
 CC octapeptide (see AAR87022), and an immunoglobulin Fc region (see
 CC AAR87023) are joined to the extracellular domain (residues 34 to 223) of
 CC the BZLF2 sequence (see AAR87020). BZLF2 proteins are members of the C-
 CC type lectin family. The C-type lectin domain is found in type II membrane
 CC proteins. The BZLF2 protein is capable of binding the beta chain of a
 CC major histocompatibility complex (MHC) class II antigen. Fusion proteins
 CC with an oligomerising zipper domain (OZD), instead of an immunoglobulin
 CC Fc region, can also be created. BZLF2 proteins inhibit antigen-specific
 CC antibody formation, proliferation of blood mononuclear cells and
 CC cytotoxic T cell responses. They also exhibit superantigen-like activity.
 CC The proteins can be used for treating or preventing autoimmune diseases
 CC such as myasthenia gravis, multiple sclerosis and systemic lupus
 CC erythematosus. Also, for treating organ or tissue transplant rejection
 CC and for treating or preventing allergy or asthma. They can be used for
 CC treating cancer and viral disease, especially EBV infection
 XX SQ Sequence 14 AA;

Query Match 92.6%; Score 50; DB 2; Length 14;
 Best Local Similarity 90.0%; Pred. No. 7;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGSSGGGGSG 10
 ||| |||||
 Db 2 GGGSGGGSG 11

Search completed: April 8, 2005, 23:31:27
 Job time : 173 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 23:25:25 ; Search time 42 Seconds
(without alignments)
17.774 Million cell updates/sec

Title: US-10-058-069-17

Perfect score: 54

Sequence: 1 GGSSGGGSG 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*

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5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	316	4	US-09-538-092-997
2	50	92.6	11	2	US-08-656-906-18
3	50	92.6	11	3	US-09-217-847-18
4	50	92.6	14	1	US-08-430-633-5
5	50	92.6	14	2	US-08-448-418-101
6	50	92.6	14	2	US-08-620-694A-5
7	50	92.6	14	2	US-08-936-854-5
8	50	92.6	14	2	US-08-656-906-26
9	50	92.6	14	3	US-09-022-255-5
10	50	92.6	14	3	US-09-022-696-5
11	50	92.6	14	3	US-09-022-253-5
12	50	92.6	14	3	US-09-022-260-5
13	50	92.6	14	3	US-09-022-259-5
14	50	92.6	14	3	US-09-022-257-5
15	50	92.6	14	3	US-09-217-847-26
16	50	92.6	14	3	US-08-849-488-16
17	50	92.6	14	4	US-09-146-979-101
18	50	92.6	14	4	US-09-125-576B-9
19	50	92.6	14	4	US-09-549-679-5
20	50	92.6	15	1	US-07-988-194A-43
21	50	92.6	15	1	US-07-843-125-13
22	50	92.6	15	1	US-08-346-293-15
23	50	92.6	15	1	US-08-164-151-23
24	50	92.6	15	1	US-08-133-804-7
25	50	92.6	15	1	US-08-331-398A-32
26	50	92.6	15	1	US-08-478-312-22
27	50	92.6	15	1	US-08-485-302-22

28 50 92.6 15 1 US-08-476-169-18 Sequence 18, Appl
29 50 92.6 15 1 US-08-484-083-18 Sequence 18, Appl
30 50 92.6 15 1 US-08-077-252B-23 Sequence 23, Appl
31 50 92.6 15 1 US-08-461-838-7 Sequence 7, Appl
32 50 92.6 15 1 US-08-575-361A-27 Sequence 27, Appl
33 50 92.6 15 2 US-08-564-955-67 Sequence 67, Appl
34 50 92.6 15 2 US-08-448-418-98 Sequence 98, Appl
35 50 92.6 15 2 US-08-461-386-7 Sequence 7, Appl
36 50 92.6 15 2 US-08-373-190-1 Sequence 1, Appl
37 50 92.6 15 2 US-08-480-774A-5 Sequence 5, Appl
38 50 92.6 15 2 US-08-356-786-14 Sequence 14, Appl
39 50 92.6 15 2 US-08-621-751A-17 Sequence 17, Appl
40 50 92.6 15 2 US-08-385-335A-7 Sequence 7, Appl
41 50 92.6 15 2 US-08-647-449-21 Sequence 21, Appl
42 50 92.6 15 2 US-08-902-623-1 Sequence 1, Appl
43 50 92.6 15 2 US-08-752-844-45 Sequence 45, Appl
44 50 92.6 15 2 US-08-465-473B-17 Sequence 17, Appl
45 50 92.6 15 2 US-08-891-848-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-09-538-092-997
; Sequence 997, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 997
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P23490
US-09-538-092-997

Query Match 100.0%; Score 54; DB 4; Length 316;

Best Local Similarity 100.0%; Pred. No. 17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGSSGGGSG 10

Db 231 GGSSGGGSG 240

RESULT 2

US-08-656-906-18
; Sequence 18, Application US/08656906
; Patent No. 5972901
; GENERAL INFORMATION:
; APPLICANT: Ferkol Jr., Thomas W.
; APPLICANT: Davis, Pamela B.
; APPLICANT: Ziady, Assem-Galal
; TITLE OF INVENTION: Serpin Enzyme Complex Receptor -
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll
; STREET: 220 Montgomery Street, Suite 2200

;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States Of America
;; ZIP: 94104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/656,906
;; FILING DATE: 03-JUN-1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/
;; FILING DATE: 03-JUN-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO WO 95/25809
;; FILING DATE: 23-MAR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/216,534
;; FILING DATE: 23-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ingolia, Diane E.
;; REGISTRATION NUMBER: 40,027
;; REFERENCE/DOCKET NUMBER: CASE-02280
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
US-08-656-906-18

Query Match 92.6%; Score 50; DB 2; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSGGGGGSG 10
Db 2 GGSGGGGGSG 11

RESULT 3
US-09-217-847-18
; Sequence 18, Application US/09217847
; Patent No. 6200801
; GENERAL INFORMATION:
; APPLICANT: Ferkol Jr., Thomas W.
; APPLICANT: Davis, Pamela B.
; APPLICANT: Ziady, Assem-Galal
; TITLE OF INVENTION: Serpin Enzyme Complex Receptor -
; TITLE OF INVENTION: Mediated Gene Transfer
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,847
; FILING DATE:

;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/656,906
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO WO 95/25809
;; FILING DATE: 23-MAR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/216,534
;; FILING DATE: 23-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ingolia, Diane E.
;; REGISTRATION NUMBER: 40,027
;; REFERENCE/DOCKET NUMBER: CASE-02280
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
US-09-217-847-18

Query Match 92.6%; Score 50; DB 3; Length 11;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSGGGGGSG 10
Db 2 GGSGGGGGSG 11

RESULT 4
US-08-430-633-5
; Sequence 5, Application US/08430633
; Patent No. 5726286
; GENERAL INFORMATION:
; APPLICANT: ALDERSON, MARK
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: COHEN, JEFFREY
; APPLICANT: COMEAU, MICHAEL
; APPLICANT: FARRAH, THERESA
; APPLICANT: SPRIGGS, MELANIE
; TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins
; TITLE OF INVENTION: That Bind MHC Class II Beta Chains
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMUNEX CORPORATION
; STREET: 51 UNIVERSITY STREET
; CITY: SEATTLE
; STATE: WASHINGTON
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple Operating System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/430,633
; FILING DATE: 28-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/235,397
; FILING DATE: 04/28/94
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2612
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Polylinker
US-08-430-633-5

Query Match 92.6%; Score 50; DB 1; Length 14;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSGGGGGSG 10
DB 2 GGSGGGGGSG 11

RESULT 5

US-08-448-418-101
Sequence 101, Application US/08448418
Patent No. 5837242
GENERAL INFORMATION:
APPLICANT: Holliger, Kaspar-Philipp
APPLICANT: Griffiths, Andrew D
APPLICANT: Hoogenboom, Hendricus RJM
APPLICANT: Malmqvist, Magnus
APPLICANT: Marks, James D
APPLICANT: McGuinness, Brian T
APPLICANT: Pope, Anthony R
APPLICANT: Prospero, Terence D
APPLICANT: Winter, Gregory P
TITLE OF INVENTION: Multivalent and Multispecific Binding
TITLE OF INVENTION: Proteins, Their Manufacture and Use
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall O'Toole Gerstein Murray and Borun
STREET: 6300 Sears Tower 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,418
FILING DATE: 14-MAY-1996
CLASSIFICATION: 435
CLASSIFICATION: C12N 15/62, 15/70, C07K 1/00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02492
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9225453.1
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9300816.7
FILING DATE: 16-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 93303614.7
FILING DATE: 10-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9319969.3
FILING DATE: 22-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32651

INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide linker
US-08-448-418-101

Query Match 92.6%; Score 50; DB 2; Length 14;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSGGGGGSG 10
DB 2 GGSGGGGGSG 11

RESULT 6

US-08-620-694A-5
Sequence 5, Application US/08620694A
Patent No. 5869286
GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: NO. 5869286el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Polylinker
US-08-620-694A-5

Query Match 92.6%; Score 50; DB 2; Length 14;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
 Db 2 GGSGGGGGSG 11

RESULT 7

US-08-936-854-5
 ; Sequence 5, Application US/08936854
 ; Patent No. 5925734
 ; GENERAL INFORMATION:
 ; APPLICANT: ALDERSON, MARK
 ; APPLICANT: ARMITAGE, RICHARD
 ; APPLICANT: COHEN, JEFFREY
 ; APPLICANT: COMEAU, MICHAEL
 ; APPLICANT: FARRAH, THERESA
 ; APPLICANT: SPRIGGS, MELANIE
 ; TITLE OF INVENTION: Isolated Epstein-Barr Virus BZLF2 Proteins
 ; TITLE OF INVENTION: That Bind MHC Class II Beta Chains
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: IMMUNEX CORPORATION
 ; STREET: 51 UNIVERSITY STREET
 ; CITY: SEATTLE
 ; STATE: WASHINGTON
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Apple Operating System 7.1
 ; SOFTWARE: Microsoft Word for Apple, Version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/936,854
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/430,633
 ; FILING DATE: 28-APR-1995
 ; APPLICATION NUMBER: 08/235,397
 ; FILING DATE: 04/28/94
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Perkins, Patricia A.
 ; REGISTRATION NUMBER: 34,693
 ; REFERENCE/DOCKET NUMBER: 2612
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206)587-0430
 ; TELEFAX: (206)233-0644
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; IMMEDIATE SOURCE:
 ; CLONE: Polylinker
 ; US-08-936-854-5

Query Match 92.6%; Score 50; DB 2; Length 14;
 Best Local Similarity 90.0%; Pred. No. 3.2;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
 Db 2 GGSGGGGGSG 11

RESULT 8

US-08-656-906-26
 ; Sequence 26, Application US/08656906
 ; Patent No. 5972901
 ; GENERAL INFORMATION:
 ; APPLICANT: Ferkol Jr., Thomas W.
 ; APPLICANT: Davis, Pamela B.

; APPLICANT: Ziady, Assem-Galal
 ; TITLE OF INVENTION: Serpin Enzyme Complex Receptor -
 ; TITLE OF INVENTION: Mediated Gene Transfer
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Medlen & Carroll
 ; STREET: 220 Montgomery Street, Suite 2200
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States Of America
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/656,906
 ; FILING DATE: 03-JUN-1996
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/
 ; FILING DATE: 03-JUN-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO 95/25809
 ; FILING DATE: 23-MAR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/216,534
 ; FILING DATE: 23-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ingolia, Diane E.
 ; REGISTRATION NUMBER: 40,027
 ; REFERENCE/DOCKET NUMBER: CASE-02280
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 705-8410
 ; TELEFAX: (415) 397-8338
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 ; MOLECULE TYPE: peptide
 ; US-08-656-906-26

Query Match 92.6%; Score 50; DB 2; Length 14;
 Best Local Similarity 90.0%; Pred. No. 3.2;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
 Db 2 GGSGGGGGSG 11

RESULT 9

US-09-022-255-5
 ; Sequence 5, Application US/09022255
 ; Patent No. 6072033
 ; GENERAL INFORMATION:
 ; APPLICANT: Yao, Zhengbin
 ; APPLICANT: Spriggs, Melanie
 ; APPLICANT: Fanslow, William
 ; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

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; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: USN 08/620,694
; APPLICATION NUMBER: USN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA: USN 08/410,535
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Polylinker
;
US-09-022-255-5

Query Match 92.6%; Score 50; DB 3; Length 14;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GGSSGGGGSG 10
Db 2 GGGGGGGSG 11

RESULT 10
US-09-022-696-5
; Sequence 5, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Polylinker
;
US-09-022-696-5

Query Match 92.6%; Score 50; DB 3; Length 14;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
Db 2 GGGGGGGSG 11

RESULT 11
US-09-022-253-5
; Sequence 5, Application US/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: No. 6096305 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Polylinker
US-09-022-253-5

Query Match 92.6%; Score 50; DB 3; Length 14;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGS GG GGS GG 10
DB 2 GGS GG GGS GG 11

RESULT 12
US-09-022-260-5
; Sequence 5, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Polylinker
US-09-022-260-5

Query Match 92.6%; Score 50; DB 3; Length 14;

Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGS GG GGS GG 10
DB 2 GGS GG GGS GG 11

RESULT 13
US-09-022-259-5
; Sequence 5, Application US/09022259
; Patent No. 6191104
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,259
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Polylinker
US-09-022-259-5

Query Match 92.6%; Score 50; DB 3; Length 14;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGS GG GGS GG 10
DB 2 GGS GG GGS GG 11

RESULT 14
US-09-022-257-5
; Sequence 5, Application US/09022257
; Patent No. 6197525

GENERAL INFORMATION:
APPLICANT: Yao, Zhengbin
APPLICANT: Spriggs, Melanie
APPLICANT: Fanslow, William
TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Power Macintosh
OPERATING SYSTEM: Apple Operating System 7.5.5
SOFTWARE: Microsoft Word for Apple, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/022,257
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/620,694
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: Polylinker
US-09-022-257-5

Query Match 92.6%; Score 50; DB 3; Length 14;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
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Db 2 GGGGGGGSG 11

RESULT 15
US-09-217-847-26
Sequence 26, Application US/09217847
Patent No. 6200801
GENERAL INFORMATION:
APPLICANT: Ferkol Jr., Thomas W.
APPLICANT: Davis, Pamela B.
APPLICANT: Ziady, Assem-Galal
TITLE OF INVENTION: Serpin Enzyme Complex Receptor -
TITLE OF INVENTION: Mediated Gene Transfer
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medien & Carroll
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California

COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,847
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/656,906
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO WO 95/25809
FILING DATE: 23-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/216,534
FILING DATE: 23-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: CASE-02280
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-09-217-847-26

Query Match 92.6%; Score 50; DB 3; Length 14;
Best Local Similarity 90.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
|||
Db 2 GGGGGGGSG 11

Search completed: April 8, 2005, 23:33:04
Job time : 43 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 23:32:26 ; Search time 141 Seconds
(without alignments)
23.546 Million cell updates/sec

Title: US-10-058-069-17

Perfect score: 54

Sequence: 1 GGSSGGGSGG 10

Scoring table: BLOSUM62

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Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	54	100.0	128	16 US-10-437-963-169578	Sequence 169578,
3	51	94.4	287	16 US-10-767-701-40206	Sequence 40206, A
4	51	94.4	559	16 US-10-437-963-187196	Sequence 187196,
5	50	92.6	12	13 US-10-081-281-38	Sequence 38, Appl
6	50	92.6	12	15 US-10-296-317-29	Sequence 29, Appl
7	50	92.6	14	9 US-09-850-715-16	Sequence 16, Appl
8	50	92.6	14	14 US-10-232-838-20	Sequence 20, Appl
9	50	92.6	14	15 US-10-363-349-5	Sequence 5, Appli
10	50	92.6	14	15 US-10-247-839-101	Sequence 101, Appl
11	50	92.6	14	15 US-10-621-693-61	Sequence 61, Appl
12	50	92.6	14	15 US-10-381-112-133	Sequence 133, Appl
13	50	92.6	14	16 US-10-742-161-5	Sequence 5, Appli

14	50	92.6	14	16	US-10-742-372-5	Sequence 5, Appli
15	50	92.6	15	9	US-09-767-395-31	Sequence 31, Appl
16	50	92.6	15	9	US-09-287-849-46	Sequence 46, Appl
17	50	92.6	15	9	US-09-147-142-29	Sequence 29, Appl
18	50	92.6	15	9	US-09-782-650-8	Sequence 8, Appli
19	50	92.6	15	9	US-09-766-543-6	Sequence 6, Appli
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23	50	92.6	15	9	US-09-911-610-5	Sequence 5, Appli
24	50	92.6	15	9	US-09-865-198-17	Sequence 17, Appl
25	50	92.6	15	9	US-09-759-352-45	Sequence 45, Appl
26	50	92.6	15	9	US-09-867-262-4	Sequence 4, Appli
27	50	92.6	15	9	US-09-747-669-7	Sequence 7, Appli
28	50	92.6	15	9	US-09-987-456-6	Sequence 6, Appli
29	50	92.6	15	9	US-09-753-126-23	Sequence 23, Appl
30	50	92.6	15	9	US-09-885-551A-4	Sequence 4, Appli
31	50	92.6	15	9	US-09-990-205-5	Sequence 5, Appli
32	50	92.6	15	9	US-09-144-886-1	Sequence 1, Appli
33	50	92.6	15	9	US-09-956-206A-67	Sequence 67, Appl
34	50	92.6	15	9	US-09-968-561A-6	Sequence 6, Appli
35	50	92.6	15	9	US-09-887-853-7	Sequence 7, Appli
36	50	92.6	15	10	US-09-939-769-96	Sequence 96, Appl
37	50	92.6	15	10	US-09-749-873-111	Sequence 111, Appl
38	50	92.6	15	10	US-09-832-355A-66	Sequence 66, Appl
39	50	92.6	15	10	US-09-896-896A-24	Sequence 24, Appl
40	50	92.6	15	10	US-09-539-382-38	Sequence 38, Appl
41	50	92.6	15	10	US-09-539-382-59	Sequence 59, Appl
42	50	92.6	15	10	US-09-798-689-17	Sequence 17, Appl
43	50	92.6	15	10	US-09-984-010-17	Sequence 17, Appl
44	50	92.6	15	10	US-09-833-041-72	Sequence 72, Appl
45	50	92.6	15	10	US-09-968-744A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-295-823-1
; Sequence 1, Application US/10295823
; Publication No. US20030157641A1
; GENERAL INFORMATION:
; APPLICANT: REFF, MITCHELL
; TITLE OF INVENTION: POLYCLONAL EXPRESSION OF ANTIBODIES
; FILE REFERENCE: 037003/291921
; CURRENT APPLICATION NUMBER: US/10/295,823
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/02373
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/US02/02374
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 60/331,481
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/400,687
; PRIOR FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 10
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: spacer peptide
US-10-295-823-1

Query Match 100.0%; Score 54; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGSGG 10
|||||

Db 1 GSSSGGGGSG 10

RESULT 2

US-10-437-963-169578
; Sequence 169578, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 169578

; LENGTH: 128

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_67986C.1.pap

US-10-437-963-169578

Query Match 100.0%; Score 54; DB 16; Length 128;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSSGGGGSG 10

Db 72 GSSSGGGGSG 81

RESULT 3

US-10-767-701-40206

; Sequence 40206, Application US/10767701

; Publication No. US20040172694A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701

; CURRENT FILING DATE: 2004-01-29

; NUMBER OF SEQ ID NOS: 63128

; SEQ ID NO 40206

; LENGTH: 287

; TYPE: PRT

; ORGANISM: Sorghum bicolor

; FEATURE:

; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C5740_1.pap

US-10-767-701-40206

Query Match 94.4%; Score 51; DB 16; Length 287;

Best Local Similarity 90.0%; Pred. No. 1.2e+02;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSSGGGGSG 10

Db 8 GSSSGGGGSG 17

RESULT 4

US-10-437-963-187196

; Sequence 187196, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 187196

; LENGTH: 559

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_83923C.1.pap

US-10-437-963-187196

Query Match 94.4%; Score 51; DB 16; Length 559;

Best Local Similarity 90.0%; Pred. No. 2.2e+02;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSSSGGGGSG 10

Db 223 GGTGGGGSG 232

RESULT 5

US-10-081-281-38

; Sequence 38, Application US/10081281

; Publication No. US20020151707A1

; GENERAL INFORMATION:

; APPLICANT: Kindvogel, Wayne

; Gross, Jane A.

; Sheppard, Paul

; TITLE OF INVENTION: Immune Mediators and Related Methods

; NUMBER OF SEQUENCES: 121

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/081,281

; FILING DATE: 20-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/261,811A

; FILING DATE: 03-Mar-1999

; APPLICATION NUMBER: US 08/480,002

; FILING DATE: 07-JUN-1995

; APPLICATION NUMBER: US 08/482,133

; FILING DATE: 07-JUN-1995

; APPLICATION NUMBER: US 08/483,241

; FILING DATE: 07-JUN-1995

; APPLICATION NUMBER: US 60/005,964

; FILING DATE: 27-OCT-1995

; APPLICATION NUMBER: US 08/657,581

; FILING DATE: 07-JUN-1996

; ATTORNEY/AGENT INFORMATION:

NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,058
REFERENCE/DOCKET NUMBER: 014058-005630US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-10-081-281-38

Query Match 92.6%; Score 50; DB 13; Length 12;
Best Local Similarity 90.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSSGGGSG 10
DB 2 GGGSGGGSG 11

RESULT 6
US-10-296-317-29
Sequence 29, Application US/10296317
Publication No. US20040057968A1
GENERAL INFORMATION:
APPLICANT: CEI-Sci Corp
APPLICANT: Zimmerman, Daniel S
APPLICANT: Sarin, Prem S
TITLE OF INVENTION: T CELL BINDING LIGAND PEPTIDES, PEPTIDE
FILE REFERENCE: CS-112
CURRENT APPLICATION NUMBER: US/10/296,317
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US 60/206548
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: PCT/US07/16793
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 96
SOFTWARE: Patent in version 3.1
SEQ ID NO 29
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide construct
US-10-296-317-29

Query Match 92.6%; Score 50; DB 15; Length 12;
Best Local Similarity 90.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSSGGGSG 10
DB 2 GGGSGGGSG 11

RESULT 7
US-09-850-715-16
Sequence 16, Application US/09850715
Patent No. US20020102656A1
GENERAL INFORMATION:
APPLICANT: Fearon, Douglas T.
APPLICANT: Dempsey, Paul W.
TITLE OF INVENTION: Modulating the Immune Response
FILE REFERENCE: A-64962/WHO/DAV
CURRENT APPLICATION NUMBER: US/09/850,715
CURRENT FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: US/08/849,488
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 1997-10-21

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9424631.1
PRIOR FILING DATE: EARLIER FILING DATE: 1994-12-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 16
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: peptides
OTHER INFORMATION: encoded by genetically engineered nucleic acids
US-09-850-715-16

Query Match 92.6%; Score 50; DB 9; Length 14;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSSGGGSG 10
DB 4 GGGSGGGSG 13

RESULT 8
US-10-232-838-20
Sequence 20, Application US/10232838
Publication No. US20030064053A1
GENERAL INFORMATION:
APPLICANT: Liu, Shengjiang
APPLICANT: Martini, Jean-Francois
APPLICANT: Liu, Dayou
TITLE OF INVENTION: MULTIVALENT PROTEIN CONJUGATE WITH MULTIPLE LIGAND-BINDING DOMAINS
FILE REFERENCE: 26050-707
CURRENT APPLICATION NUMBER: US/10/232,838
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 06/316,718
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent in version 3.1
SEQ ID NO 20
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Linker
US-10-232-838-20

Query Match 92.6%; Score 50; DB 14; Length 14;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSSSGGGSG 10
DB 2 GGGSGGGSG 11

RESULT 9
US-10-363-349-5
Sequence 5, Application US/10363349
Publication No. US2004005329A1
GENERAL INFORMATION:
APPLICANT: Kontermann, Roland
APPLICANT: Miller, Daniel
APPLICANT: Muller, Rolf
TITLE OF INVENTION: Endoglin-Specific Polypeptide, Production and Use Thereof
FILE REFERENCE: BB-104
CURRENT APPLICATION NUMBER: US/10/363,349
CURRENT FILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: PCT/EP01/10197
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: DE 100 43 481.9
PRIOR FILING DATE: 2000-09-04
NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: linker peptide
US-10-363-349-5

Query Match 92.6%; Score 50; DB 15; Length 14;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
|||
Db 1 GGSSGGGGSG 10

RESULT 10
US-10-247-839-101
Sequence 101, Application US/10247839
Publication No. US20040058400A1

GENERAL INFORMATION:
APPLICANT: Holliger, Kaspar-Philipp
Griffiths, Andrew D
Hoogenboom, Hendricus RJM
Malmqvist, Magnus
Marks, James D
McGuinness, Brian T
Pope, Anthony R
Prospero, Terence D
Winter, Gregory P
TITLE OF INVENTION: Multivalent and Multispecific Binding
Proteins, Their Manufacture and Use

NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshall O'Toole Gerstein Murray and Borun
STREET: 6300 Sears Tower 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/247,839
FILING DATE: 20-Sep-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/146,979
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/448,418
FILING DATE: 14-MAY-1996
APPLICATION NUMBER: PCT/GB93/02492
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: GB 9225453.1
FILING DATE: 04-DEC-1992
APPLICATION NUMBER: GB 9300816.7
FILING DATE: 16-JAN-1993
APPLICATION NUMBER: EP 93303614.7
FILING DATE: 10-MAY-1993
APPLICATION NUMBER: GB 9319969.3
FILING DATE: 22-SEP-1993

ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32651
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide linker
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-247-839-101

Query Match 92.6%; Score 50; DB 15; Length 14;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
|||
Db 2 GGSSGGGGSG 11

RESULT 11
US-10-621-693-61
Sequence 61, Application US/10621693
Publication No. US20040059093A1
GENERAL INFORMATION:
APPLICANT: Gentide Biopharmaceuticals, Inc.
APPLICANT: Busseil, Stuart
TITLE OF INVENTION: METHODS TO CONSTRUCT MULTIMERIC DNA AND POLYMERIC PROTEIN SEQUENCES
FILE REFERENCE: GNT-00101.P.1-US
CURRENT APPLICATION NUMBER: US/10/621,693
CURRENT FILING DATE: 2003-07-16
PRIOR APPLICATION NUMBER: US 60/396,466
PRIOR FILING DATE: 2002-07-16
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PatentIn version 3.0
SEQ ID NO 61
LENGTH: 14

TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: synthetic sequence
US-10-621-693-61

Query Match 92.6%; Score 50; DB 15; Length 14;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
|||
Db 2 GGSSGGGGSG 11

RESULT 12
US-10-381-112-133
Sequence 133, Application US/10381112
Publication No. US20040086942A1
GENERAL INFORMATION:
APPLICANT: Lowman, Henry B.
APPLICANT: Nakamura, Gerald R.
APPLICANT: Reynolds, Mark E.
APPLICANT: Starovasinik, Melissa A.
TITLE OF INVENTION: IGE RECEPTOR ANTAGONISTS
FILE REFERENCE: P1816R1
CURRENT APPLICATION NUMBER: US/10/381,112
CURRENT FILING DATE: 2003-10-27
PRIOR APPLICATION NUMBER: US 60/278,540
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/235,353
PRIOR FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 595
SEQ ID NO 133
LENGTH: 14

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: linker connecting Ige120 to g3p phage sequence
US-10-381-112-133

Query Match 92.6%; Score 50; DB 15; Length 14;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
||| |||||
Db 1 GGSSGGGGSG 10

RESULT 13

US-10-742-161-5
; Sequence 5, Application US/10742161
; Publication No. US20040120898A1
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; Spriggs, Melanie
; Fanelow, William
; TITLE OF INVENTION: Novel Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/742,161
; FILING DATE: 18-Dec-2003
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: Not Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Polylinker
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-742-161-5

Query Match 92.6%; Score 50; DB 16; Length 14;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
||| |||||
Db 2 GGSSGGGGSG 11

RESULT 14

US-10-742-372-5

; Sequence 5, Application US/10742372
; Publication No. US20040120899A1
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; Spriggs, Melanie
; Fanelow, William
; TITLE OF INVENTION: Novel Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/742,372
; FILING DATE: 18-Dec-2003
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)

INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: Not Relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: Polylinker
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-742-372-5

Query Match 92.6%; Score 50; DB 16; Length 14;
Best Local Similarity 90.0%; Pred. No. 13;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
||| |||||
Db 2 GGSSGGGGSG 11

RESULT 15

US-09-767-395-31
; Sequence 31, Application US/09767395
; Patent No. US20020004215A1
; GENERAL INFORMATION:

APPLICANT: Osbourn, Jane K
; Derbyshire, Elaine J
; McCafferty, John G
; Vaughan, Tristan J
; Johnson, Kevin S
; TITLE OF INVENTION: Labelling and selection of molecules
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/767,395
FILING DATE: 23-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/098,244
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/GB97/01835
FILING DATE: 08-JUL-1997
APPLICATION NUMBER: GB 9614292.2
FILING DATE: 08-JUL-1996
APPLICATION NUMBER: GB 9624880.2
FILING DATE: 29-NOV-1996
APPLICATION NUMBER: GB 9712818.5
FILING DATE: 18-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/34800
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-767-395-31

Query Match 92.6%; Score 50; DB 9; Length 15;
Best Local Similarity 90.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGSSGGGGSG 10
Db 2 GGSSGGGGSG 11

Search completed: April 8, 2005, 23:47:34
Job time : 142 secs

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OM protein - protein search, using sw model

Run on: April 8, 2005, 23:17:04 ; Search time 43 Seconds
(without alignments)
22.376 Million cell updates/sec

Title: US-10-058-069-17
Perfect score: 54
Sequence: 1 GGSSGGGGSG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	54	100.0	316	1	loricrin - human
2	54	100.0	581	1	keratin, type II c
3	54	100.0	722	1	coat protein VP1 -
4	50	92.6	183	2	keratin-like prote
5	50	92.6	249	2	single chain Fv an
6	50	92.6	257	2	hypothetical prote
7	50	92.6	259	2	hypothetical prote
8	50	92.6	328	2	protein K04G7.10 l
9	50	92.6	358	2	hypothetical prote
10	50	92.6	371	2	hypothetical prote
11	50	92.6	433	2	homeotic protein H
12	50	92.6	481	2	loricrin - mouse
13	50	92.6	596	1	keratins, 54K type
14	50	92.6	528	2	hypothetical prote
15	50	92.6	592	2	endo-1,4-beta-gluc
16	50	92.6	593	1	keratin 10, type I
17	50	92.6	633	2	probable protein k
18	50	92.6	639	2	dnak-type molecula
19	50	92.6	737	2	DNA-binding protei
20	50	92.6	1053	2	reverse transcript
21	50	92.6	1969	2	histidine kinase h
22	50	92.6	2038	2	female sterile hom
23	49	90.7	1093	2	AF17 protein - hum
24	48	88.9	296	2	RNA-binding protei
25	48	88.9	296	2	gene Merc protein
26	48	88.9	347	2	channel protein vi
27	48	88.9	382	2	hypothetical membr
28	48	88.9	382	2	hypothetical prote
29	48	88.9	434	1	coat protein A - p

30	48	88.9	495	2	B71360	hypothetical prote
31	48	88.9	561	2	A31994	keratin 10, type I
32	48	88.9	569	1	KRMSE1	keratin, 59K type
33	48	88.9	570	2	S07330	keratin, epidermal
34	48	88.9	622	2	I37984	keratin 9, type I
35	48	88.9	877	2	T43449	hypothetical prote
36	48	88.9	1146	2	A55332	myosin-heavy-chain
37	47	87.0	174	2	E84868	hypothetical prote
38	47	87.0	299	2	T00837	glycine-rich prote
39	47	87.0	312	2	JN0451	phosphoribosylanth
40	47	87.0	339	2	S20880	homeotic protein H
41	47	87.0	342	2	S14432	heterogeneous ribo
42	47	87.0	389	2	D28995	homeotic protein U
43	47	87.0	399	2	I49754	homeobox protein -
44	47	87.0	484	2	G70846	hypothetical glyci
45	47	87.0	531	2	S09859	hypothetical prote

ALIGNMENTS

RESULT 1

A38743
loricrin - human
C:Species: Homo sapiens (man)
C:Date: 20-Sep-1991 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C:Accession: A38743; A43410
R:Hoehl, D.; Mehrel, T.; Lichti, U.; Turner, M.L.; Roop, D.R.; Steinert, P.M.
J. Biol. Chem. 266, 6626-6636, 1991
A:Title: Characterization of human loricrin. Structure and function of a new class of e;
A:Reference number: A38743; MUID:9117926; PMID:2007607
A:Accession: A38743
A:Molecule type: mRNA
A:Residues: 1-316 <OH>
A:Cross-references: UNIPROT:P23490; GB:M61120; NID:g187184; PIDN:AAA36180.1; PID:g18718
A:Note: Translation of Met-1 is not shown
R:Yoneda, K.; Hoehl, D.; McBride, O.W.; Wang, M.; Cehrs, K.U.; Idler, W.W.; Steinert, P.
J. Biol. Chem. 267, 18060-18066, 1992
A:Title: The human loricrin gene.
A:Reference number: A43410; MUID:92388173; PMID:1355480
A:Accession: A43410
A:Molecule type: DNA
A:Residues: 2-151, 'C', 153-232, 'C', 234-316 <YON>
A:Cross-references: GB:M94077; NID:g187186; PIDN:AAA36181.1; PID:g187187
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:112880, NCBIP:112882)
C:Comment: During the terminal differentiation of epidermal (stratum corneum) cell, thi
n insoluble, cross-linked envelope (the cornified cell envelope) under the plasma membr
C:Genetics:
A:Gene: GDB:LOR
A:Cross-references: GDB:132049; OMIM:152445
A:Map position: 1q21-1q21
A:Introns: #status absent
C:Superfamily: loricrin
C:Keywords: cornified cell envelope; disulfide bond; duplication; epidermis; tandem rep
F:89/Cross-link: isopeptide (Lys) (interchain to Gln-154) (partial) #status experimenta
F:89/Cross-link: isopeptide (Lys) (interchain to Gln-220) (partial) #status experimenta
F:154/Cross-link: isopeptide (Gln) (interchain to Lys-89) #status experimental
F:216/Cross-link: isopeptide (Gln) (interchain to Lys-316) #status experimental
F:220/Cross-link: isopeptide (Gln) (interchain to Lys-89) #status experimental
F:316/Cross-link: isopeptide (Lys) (interchain to Gln-216) (partial) #status experiment

Query Match 100.0%; Score 54; DB 1; Length 316;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10

DB 231 GGSSGGGGSG 240

RESULT 2

KRMS2
keratin, type II cytoskeletal - mouse (fragment)
N:Alternate names: 67-kDa type II keratin
C:Species: Mus musculus (house mouse)
C>Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C:Accession: A02951
R:Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.
J. Biol. Chem. 260, 7142-7149, 1985
A:Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67,000
late filament subunits.
A:Reference number: A92535; MUID:85207740; PMID:2581964
A:Accession: A02951
A:Molecule type: mRNA
A:Residues: 1-581 <STE>
A:Cross-references: UNIPROT:P04104; GB:M10937; NID:g198622; PID:g387396
C:Superfamily: cytoskeletal keratin
C:Keywords: coiled coil; intermediate filament
F:1-106/Domain: head (fragment) <HED>
F:1-106/Region: V1 subdomain (fragment)
F:71-106/Region: H1 subdomain
F:107-419/Domain: rod <ROD>
F:107-141/Region: coil 1A
F:142-153/Region: linker 1
F:154-254/Region: coil 1B
F:255-271/Region: linker 12
F:272-290/Region: coil 2A
F:291-298/Region: linker 2
F:299-419/Region: coil 2B
F:357/Region: stutter
F:420-581/Domain: tail <END>
F:420-439/Region: H2 subdomain
F:440-581/Region: V2 and E2 subdomains

Query Match 100.0%; Score 54; DB 1; Length 581;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
|||
Db 496 GGSSGGGGSG 505

RESULT 3
VCPW2
coat protein VP1 - parvovirus H1
C:Species: parvovirus H1
A:Note: host Homo sapiens (man)
C>Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C:Accession: A03699
R:Rhode III, S.L.; Paradiso, P.R.
J. Virol. 45, 173-184, 1983
A:Title: Parvovirus genome: nucleotide sequence of H-1 and mapping of its genes by hybridization
A:Reference number: A03699; MUID:83112183; PMID:6823009
A:Accession: A03699
A:Molecule type: DNA
A:Residues: 1-722 <RHO>
A:Cross-references: UNIPROT:P03136; EMBL:X01457; EMBL:J02198
C:Superfamily: parvovirus coat protein
C:Keywords: coat protein

Query Match 100.0%; Score 54; DB 1; Length 722;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
|||
Db 156 GGSSGGGGSG 165

RESULT 4
PNO109
keratin-like protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997
C:Accession: PNO109
R:Shvets, Y.P.; Chumakov, I.M.; Kisselev, L.L.
Mol. Biol. 24, 663-677, 1990
A:Title: Sequencing the fragment from a transcriptionally active rat genomic locus and its subclones.
A:Reference number: PNO109
A:Accession: PNO109
A:Molecule type: mRNA
A:Residues: 1-183 <SHV>
C:Genetics:
A:Gene: K51
C:Superfamily: loricrin
C:Keywords: duplication
F:21-28/Region: 8-residue repeat
F:34-41/Region: 8-residue repeat
F:73-88/Region: 16-residue repeat
F:77-84/Region: 8-residue repeat
F:89-104/Region: 16-residue repeat
F:93-100/Region: 8-residue repeat
F:105-112/Region: 8-residue repeat
F:118-125/Region: 8-residue repeat
F:152-163/Region: 12-residue repeat
F:152-159/Region: 8-residue repeat
F:164-175/Region: 12-residue repeat
F:164-171/Region: 8-residue repeat
F:176-183/Region: 8-residue repeat

Query Match 92.6%; Score 50; DB 2; Length 183;
Best Local Similarity 90.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
|||
Db 124 GGSSGGGGSG 133

RESULT 5
S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A:Description: Construction and functional characterization of a single chain Fv antibody
A:Reference number: S41374
A:Accession: S41374
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL:Z29480

Query Match 92.6%; Score 50; DB 2; Length 249;
Best Local Similarity 90.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
|||
Db 121 GGSSGGGGSG 130

RESULT 6
C84890
hypothetical protein At2g45420 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: C84890
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.; Euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: C84890
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <STO>
A:Cross-references: GB:AE002093; NID:g2583113; PIDN:AAB82622.1; GSPDB:GN00139
C:Genetics:
A:Gene: A2g45420
A:Map position: 2

Query Match 92.6%; Score 50; DB 2; Length 257;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GGSSGGGGGG 10
|||||
DB 27 GGSSGGGGGG 36

RESULT 7
F86475
hypothetical protein F12A4.2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F86475
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; Ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurob, J.S.; Mafti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F86475
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <STO>
A:Cross-references: UNIPROT:Q9C8P8; GB:AE005172; NID:g10092190; PIDN:AAG12608.1; GSPDB:G
C:Genetics:
A:Map position: 1

Query Match 92.6%; Score 50; DB 2; Length 259;
Best Local Similarity 90.0%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GGSSGGGGGG 10
|||||
DB 8 GGSSGGGGGG 17

RESULT 8
G88499
protein K04G7.10 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G88499
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: G88499
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-328 <STO>
A:Cross-references: UNIPROT:Q09584; GB:chr_III; PIDN:AAA62536.1; PID:g687845; GSPDB:GN00
C:Genetics:
A:Gene: K04G7.10
A:Map position: 3

Query Match 92.6%; Score 50; DB 2; Length 328;
Best Local Similarity 90.0%; Pred. No. 21;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GGSSGGGGGG 10
|||||
DB 313 GGSSGGGGGG 322

RESULT 9
T26281
hypothetical protein W08D2.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26281
R:Swinburne, J.; Ainscough, R.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z20188
A:Accession: T26281
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-358 <WIL>
A:Cross-references: UNIPROT:Q23222; EMBL:Z70271; PIDN:CAA94234.1; GSPDB:GN00022; CESP:W0
C:Genetics:
A:Experimental source: clone W08D2
A:Gene: CESP:W08D2.6
A:Map position: 4
A:Introns: 57/3; 320/2

Query Match 92.6%; Score 50; DB 2; Length 358;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GGSSGGGGGG 10
|||||
DB 332 GGSSGGGGGG 341

RESULT 10
T13021
hypothetical protein F8L21.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13021
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Me:
submitted to the Protein Sequence Database, July 1999
A:Reference number: Z17587
A:Accession: T13021
A:Molecule type: DNA
A:Residues: 1-371 <BEV>
A:Cross-references: UNIPROT:Q9SUT1; EMBL:AL096882; GSPDB:GN00062; ATSP:F8L21.90
A:Experimental source: cultivar Columbia; BAC clone F8L21
C:Genetics:
A:Gene: ATSP:F8L21.90
A:Map position: 4

Query Match 92.6%; Score 50; DB 2; Length 371;
Best Local Similarity 90.0%; Pred. No. 23;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 GGSSGGGGGG 10
|||||
DB 193 GGSSGGGGGG 202

RESULT 11
S20963
homeotic protein Hox B3 - mouse
N:Alternate names: homeotic protein Hox 2.7
C:Species: Mus musculus (house mouse)
C:Date: 22-Nov-1993 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S20963; D42694
R:Sham, M.H.; Hunt, P.; Nonchev, S.; Papalopulu, N.; Graham, A.; Boncinelli, E.; Krumian

EMBO J. 11, 1825-1836, 1992
 A;Title: Analysis of the murine Hox-2.7 gene: conserved alternative transcripts with dif
 A;Reference number: S20963; MUID:92258392; PMID:1582411
 A;Accession: S20963
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-433 <SHA>
 A;Cross-references: UNIPROT:P09026; GB:X66177; GB:S35628; NID:g312229; PIDN:O
 R;Nazari, A.; Kim, Y.; Nirenberg, M.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2883-2887, 1992
 A;Title: Hox-1.11 and Hox-4.9 homeobox genes.
 A;Reference number: A42694; MUID:92212934; PMID:1348361
 A;Accession: D42694
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 213-238 <NAZ>
 A;Note: sequence extracted from NCBI backbone (NCBIN:92310, NCBI:P.92316)
 C;Superfamily: homeotic protein Hox B3; homeobox homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;192-248/Domain: homeobox homology <HOX>

Query Match 92.6%; Score 50; DB 2; Length 433;
 Best Local Similarity 90.0%; Pred. No. 26;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGGG 10
 |||||
 Db 168 GGSSGGGGGG 177

RESULT 12

A35628
 loricrin - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 09-Jul-2004
 C;Accession: A35628
 R;Mehrel, T.; Hohl, D.; Rothnagel, J.A.; Longley, M.A.; Bundman, D.; Cheng, C.; Lichti,
 Cell 61, 1103-1112, 1990
 A;Title: Identification of a major keratinocyte cell envelope protein, loricrin.
 A;Reference number: A35628; MUID:90275605; PMID:2190691
 A;Accession: A35628
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-481 <MEH>
 A;Cross-references: UNIPROT:P18165; GB:M34398; NID:g198870; PIDN:AAA3444.1; PID:g198871
 C;Superfamily: loricrin
 C;Keywords: cornified cell envelope; epidermis

Query Match 92.6%; Score 50; DB 2; Length 481;
 Best Local Similarity 90.0%; Pred. No. 29;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGGG 10
 |||||
 Db 159 GGSSGGGGGG 168

RESULT 13

KRBOVI
 keratin, 54K type I cytoskeletal - bovine
 N;Alternate names: 54-kDa type I keratin; cytokeratin Vlb
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
 C;Accession: A02941; S07262
 R;Rieger, M.; Jorcano, J.L.; Franke, W.W.
 EMBO J. 4, 2261-2267, 1985
 A;Title: Complete sequence of a bovine type I cytokeratin gene: conserved and variable
 A;Reference number: A02941; MUID:86081734; PMID:2416562
 A;Accession: A02941
 A;Molecule type: DNA
 A;Residues: 1-526 <RIE>
 A;Cross-references: UNIPROT:P06394; GB:X02870; NID:g478; PIDN:CAA26626.1; PID:g479
 R;Jorcano, J.L.; Rieger, M.; Franz, J.K.; Schiller, D.L.; Moll, R.; Franke, W.W.

J. Mol. Biol. 179, 257-281, 1984
 A;Title: Identification of two types of keratin polypeptides within the acidic cytoke
 A;Reference number: S07262; MUID:85058191; PMID:6209405
 A;Accession: S07262
 A;Molecule type: mRNA
 A;Residues: 281-466, 'PAAATAAEVQRPRRFRQYG', 490-491, 494, 'PVAVARRK', 504-526 <JOR>
 A;Cross-references: EMBL:X01460
 A;Note: this sequence has been revised in reference A02941
 C;Genetics:

A;Gene: cytokeratin Vlb
 A;Introns: 190/3; 218/2; 270/3; 324/3; 366/3; 439/2; 525/2
 C;Superfamily: cytoskeletal keratin
 C;Keywords: coiled coil; intermediate filament
 F;1-127/Domain: head <HED>
 F;1-127/Region: E1 and V1 subdomains
 F;128-441/Domain: rod <ROD>
 F;128-162/Region: coil 1A
 F;163-176/Region: linker 1
 F;177-277/Region: coil 1B
 F;278-293/Region: linker 12
 F;294-312/Region: coil 2A
 F;313-320/Region: linker 2
 F;321-441/Region: coil 2B
 F;379/Region: stutter
 F;442-526/Domain: tail <END>
 F;442-526/Region: V2 and E2 subdomains

Query Match 92.6%; Score 50; DB 1; Length 526;
 Best Local Similarity 90.0%; Pred. No. 31;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGGG 10
 |||||
 Db 452 GGSSGGGGGG 461

RESULT 14

D46449
 hypothetical protein TrbL [imported] - plasmid RK2
 C;Species: plasmid RK2
 C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 02-Jun-2000
 C;Accession: D46449
 R;Lessl, M.; Balzer, D.; Pansegrau, W.; Lanka, E.
 J. Biol. Chem. 267, 20471-20480, 1992
 A;Title: Sequence similarities between the RP4 Tra2 and the Ti VirB region strongly sup
 A;Reference number: A44020; MUID:93015931; PMID:1400366
 A;Contents: incompatibility group P
 A;Accession: D46449

A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-528 <LES>
 A;Cross-references: GB:M93696; NID:g152554; PIDN:AAA26438.1; PID:g152566
 A;Note: sequence extracted from NCBI backbone (NCBIP:115786)
 C;Genetics:
 A;Genome: plasmid

Query Match 92.6%; Score 50; DB 2; Length 528;
 Best Local Similarity 90.0%; Pred. No. 32;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGGG 10
 |||||
 Db 368 GGSSGGGGGG 377

RESULT 15

E82759
 endo-1,4-beta-glucanase XF0818 [imported] - Xylella fastidiosa (strain 9a5c)
 C;Species: Xylella fastidiosa
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: E82759
 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82759
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-592 <SIM>
A;Cross-references: UNIPROT:Q9PFF60; GB:AE003849; NID:99105710; PIDN:AAF8362
A;Experimental source: strain 9a5C
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF0818

Query Match 92.6%; Score 50; DB 2; Length 592;
Best Local Similarity 90.0%; Pred. No. 35;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGSSGGGGG 10
|||
Db 468 GGSGGGGGG 477

Search completed: April 8, 2005, 23:32:17
Job time : 45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 8, 2005, 23:26:05 ; Search time 176 Seconds
(without alignments)
29.095 Million cell updates/sec

Title: US-10-058-069-17
Perfect score: 54
Sequence: 1 GGSSGGGGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	316	1 LORI HUMAN	P23490 homo sapien
2	54	100.0	316	2 Q6FHY3	Q6fhy3 homo sapien
3	54	100.0	627	1 K2C1 MOUSE	P04104 mus musculus
4	54	100.0	637	2 Q9D2K8	Q9d2k8 mus musculus
5	54	100.0	722	1 COAT_PAVH	P03136 hamster par
6	54	100.0	893	2 Q7XHW2	Q7xhw2 oryza sativ
7	51	94.4	239	2 Q9VVR9	Q9vvr9 drosophila
8	51	94.4	256	2 Q9L7V8	Q9l7v8 haemophilus
9	51	94.4	292	2 Q702C2	Q702c2 uncultured
10	51	94.4	455	2 Q8F1W0	Q8f1w0 leptospira
11	51	94.4	465	1 FXD3 MOUSE	Q61060 mus musculus
12	51	94.4	559	2 Q8S0K8	Q8s0k8 oryza sativ
13	51	94.4	582	2 Q7PWR9	Q7pwr9 anopheles g
14	51	94.4	950	2 Q923A9	Q923a9 mus musculus
15	51	94.4	1062	2 Q9NHD3	Q9nhd3 drosophila
16	51	94.4	1232	2 Q6CGJ6	Q6cgj6 yarrowia li
17	51	94.4	2157	2 Q9Z1R1	Q9z1r1 mus musculus
18	51	94.4	2158	2 Q7TSC1	Q7tsc1 mus musculus
19	51	94.4	2161	2 Q6MG48	Q6mg48 rattus norv
20	50	92.6	144	2 Q7PJ48	Q7pj48 anopheles g
21	50	92.6	155	2 Q80WU5	Q80wu5 mus musculus
22	50	92.6	170	2 Q92S52	Q92s52 mus musculus
23	50	92.6	173	2 Q6UIP1	Q6uip1 macaca mula
24	50	92.6	174	2 Q6UIP2	Q6uip2 pan troglod
25	50	92.6	191	2 Q46029	Q46029 chironomus
26	50	92.6	193	2 Q7XDR9	Q7xdr9 oryza sativ
27	50	92.6	213	2 Q6A134	Q6a134 homo sapien
28	50	92.6	218	2 Q92S51	Q92s51 mus musculus
29	50	92.6	239	2 Q69T79	Q69t79 oryza sativ
30	50	92.6	240	2 Q65ZC9	Q65zc9 homo sapien
31	50	92.6	241	2 Q921A6	Q921a6 mus musculus

32	50	92.6	243	2 Q7TQM2	Q7tqm2 mus musculus
33	50	92.6	244	2 Q65ZC8	Q65zc8 homo sapien
34	50	92.6	248	2 Q65ZQ7	Q65zq7 mus sp. b3(
35	50	92.6	255	2 Q6KB05	Q6kb05 mus musculus
36	50	92.6	256	2 Q8S2J0	Q8s2j0 oryza sativ
37	50	92.6	259	2 Q9C8P8	Q9c8p8 arabidopsis
38	50	92.6	262	1 LB18 ARATH	Q22131 arabidopsis
39	50	92.6	262	2 Q65Z11	Q65z11 mus musculus
40	50	92.6	278	2 Q6JBL3	Q6jbl3 zea mays (s
41	50	92.6	278	2 Q6JBL5	Q6jbl5 zea mays (s
42	50	92.6	287	2 Q6GLA3	Q6gl3 xenopus tro
43	50	92.6	298	2 Q9QYF0	Q9qyf0 synthetic c
44	50	92.6	306	1 R4LY HUMAN	Q9ukm9 homo sapien
45	50	92.6	316	2 Q81FW7	Q81fw7 chironomus

ALIGNMENTS

RESULT 1					
ID	LORI HUMAN	STANDARD;	PRT;	316 AA.	
AC	P23490;				
DT	01-NOV-1991 (Rel. 20, Created)				
DT	01-NOV-1991 (Rel. 20, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	Loricrin.				
GN	Name=LOR; Synonyms=LRN;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND GLN-LYS CROSSLINKS.				
RC	TISSUE=Foreskin;				
RX	MEDLINE=91177926; PubMed=2007607;				
RA	Hohl D., Mehrel T., Lichti U., Turner M.L., Roop D.R., Steinert P.M.;				
RT	"Characterization of human loricrin. Structure and function of a new				
RT	class of epidermal cell envelope proteins.";				
RL	J. Biol. Chem. 266:6626-6636(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=92388173; PubMed=1355480;				
RA	Yoneda K., Hohl D., McBride O.W., Wang M., Cehrs K.U., Idler W.W.,				
RA	Steinert P.M.;				
RT	"The human loricrin gene.";				
RL	J. Biol. Chem. 267:18060-18066(1992).				
RN	[3]				
RP	GLN-LYS CROSSLINKS WITH SPRR PROTEINS.				
RX	PubMed=10066784; DOI=10.1074/jbc.274.11.7226;				
RA	Candi E., Tarcea E., Idler W.W., Kartasova T., Marekov L.N.,				
RA	Steinert P.M.;				
RT	Transglutaminase cross-linking properties of the small proline-rich 1				
RT	family of cornified cell envelope proteins. Integration with				
RT	loricrin.";				
RL	J. Biol. Chem. 274:7226-7237(1999).				
RN	[4]				
RP	DISEASE.				
RX	PubMed=12072018;				
RA	O'Driscoll J., Muston G.C., McGrath J.A., Lam H.M., Ashworth J.,				
RA	Christiano A.M.;				
RT	"A recurrent mutation in the loricrin gene underlies the ichthyotic				
RT	variant of Volvinkel syndrome.";				
RL	Clin. Exp. Dermatol. 27:243-246(2002).				
RN	[5]				
RP	DISEASE.				
RX	PubMed=12615358; DOI=10.1016/S0923-1811(02)00143-3;				
RA	Ishida-Yamamoto A.;				
RA	"Loricrin keratoderma: a novel disease entity characterized by nuclear				
RT	accumulation of mutant loricrin.";				
RL	J. Dermatol. Sci. 31:3-8(2003).				
CC	-1- FUNCTION: Major keratinocyte cell envelope protein.				
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic and nucleoplasmic.				

CC -I- PTM: Substrate of transglutaminases. Some glutamines and lysines
 CC are crosslinked to other loricrin molecules and to SPRRs proteins.
 CC -I- PTM: Contains inter- or intramolecular disulfide-bonds (Probable).
 CC -I- DISEASE: Defects in LOR are the cause of loricrin keratoderma (LK)
 CC [MIM:604117]. LK is an ichthyotic variant of Vohwinkel syndrome
 CC (VS) characterized by progressive symmetric erythrokeratoderma or
 CC congenital ichthyosiform erythroderma born as a collodion baby.
 CC Common clinical features include hyperkeratosis of the palms and
 CC soles with digital constriction. In all form of LK, the defects
 CC are caused by single allele mutations and are caused by nucleotide
 CC insertions. These frameshift mutations produce longer mutant
 CC proteins with a C-terminus rich in Arg containing potential
 CC bipartite NLSs. The mutant loricrin is nuclear.
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 CC -----

DR EMBL; M61120; AAA36180.1; -;
 DR EMBL; M94077; AAA36181.1; -;
 DR PIR; A38743; A38743.
 DR Genew; HGNC:6663; LOR.
 DR MIM; 152445; -;
 DR MIM; 604117; -;
 DR GO; GO:0005626; C:insoluble fraction; TAS.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; TAS.
 KW Direct protein sequencing; Keratinization; Repeat; Structural protein.
 FT CROSSLINK 89 220 Iso-glutamyl lysine isopeptide (Lys-Gln).
 FT CROSSLINK 157 316 Iso-glutamyl lysine isopeptide (Gln-Lys).
 SQ SEQUENCE 316 AA; 26033 MW; 100FEC52F9ACE8E CRC64;

Query Match 100.0%; Score 54; DB 1; Length 316;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
 DB 231 GGSSGGGGSG 240

RESULT 2

Q6FHY3 PRELIMINARY; PRT; 316 AA.
 AC Q6FHY3;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE LOR protein.
 GN Homo-LOR;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Halleck A., Ebert L., Mkundinya M., Schick M., Eisenstein S.,
 RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
 RA Korn B., Zuo D., Hu Y., LaBaer J.,
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR536555; CAG38792.1; -;
 DR InterPro; IPR002952; Eggshell.
 DR PRINTS; PR01228; EGGSHL.
 SQ SEQUENCE 316 AA; 26019 MW; A14AF9001A04B58F CRC64;

Query Match 100.0%; Score 54; DB 2; Length 316;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10

Db 231 GGSSGGGGSG 240

RESULT 3

K2C1 MOUSE
 ID K2C1 MOUSE STANDARD; PRT; 627 AA.
 AC P04104;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Keratin, type II cytoskeletal 1 (Cytokeratin 1) (67 kDa cytoke-
 GN Name=Krt1; Synonyms=Krt2-1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 83-628 FROM N.A.
 RX MEDLINE=85207740; PubMed=2581964;
 RA Steinert P.M., Parry D.A.D., Idler W.W., Johnson L.D., Steven A.C.,
 RA Roop D.R.;
 RT "Amino acid sequences of mouse and human epidermal type II keratins of
 RT Mr 67,000 provide a systematic basis for the structural and functional
 RT diversity of the end domains of keratin intermediate filament
 RT subunits.";
 RL J. Biol. Chem. 260:7142-7149(1985).
 RN [2]
 RP SEQUENCE FROM N.A., AND REVISIONS.
 RA Roop D.R.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -I- SUBUNIT: Heterotetramer of two type I and two type II keratins.
 CC -I- MISCELLANEOUS: There are two types of cytoskeletal and
 CC microfibrillar keratin, I (acidic) and II (neutral to basic) (40-
 CC 55 and 56-70 kilodaltons, respectively). filament family.
 CC -I- SIMILARITY: Belongs to the intermediate filament family.
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 CC -----

DR EMBL; M10937; AAD05191.1; -;
 DR PIR; A02951; KEMS2.
 DR HSP; P08670; IKG7.
 DR SWISS-2DPAGE; P04104; MOUSE.
 DR MGD; MGI:96698; Krt2-1.
 DR InterPro; IPR011000; ApoLp_III_like.
 DR InterPro; IPR001664; IF.
 DR InterPro; IPR003054; Keratin_II.
 DR Pfam; PF00038; Filament; 1.
 DR PRINTS; PR01276; TYPE2KERATIN.
 DR PROSITE; PS00226; IF; 1.
 KW Coiled coil; Intermediate filament; Keratin.
 RN INIT MET 0 By similarity.
 FT DOMAIN 1 186 Head.
 FT DOMAIN 187 496 Rod.
 FT DOMAIN 497 627 Tail.
 FT DOMAIN 187 222 Coiled 1A.
 FT DOMAIN 223 242 Linker 1.
 FT DOMAIN 243 333 Coiled 1B.
 FT DOMAIN 334 357 Linker 12.
 FT DOMAIN 358 496 Coiled 2.
 FT SITE 451 451 Stutter.
 SQ SEQUENCE 627 AA; 65092 MW; EF7E848654539578 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 627;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGSSGGGGSG 10
DB 550 GGSSGGGGSG 559

RESULT 4
Q9D2K8 PRELIMINARY; PRT; 637 AA.
AC Q9D2K8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonatal head cDNA, RIKEN full-length enriched
DE library, clone:4833436C19 product:keratin complex 2, basic, gene 1,
DE full insert sequence.
GN Name=Krt2-1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6979(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=20330913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Iehi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hangaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

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RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the intermediate filament family.
DR EMBL; AK019521; BAB31776.1; -.
DR HSSP; P08670; 1GK7.
DR MGD; MGI:96698; Krt2-1.
DR GO; GO:0005882; C:intermediate filament; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR011000; Apolp_III_like.
DR InterPro; IPR001664; IF.
DR InterPro; IPR002957; Keratin I.
DR InterPro; IPR003054; Keratin II.
DR Pfam; PF00038; Filament; 1.
DR PRINTS; PRO1248; TYPE1KERATIN.
DR PRINTS; PRO1276; TYPE2KERATIN.
DR PROSITE; PS00226; IF; 1.
KW Intermediate filament; Keratin.
SQ SEQUENCE 637 AA; 65627 MW; D6344FDD0468EAC7 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 637;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
DB 551 GGSSGGGGSG 560

RESULT 5
COAT_PAVHH
ID COAT_PAVHH STANDARD; PRT; 722 AA.
AC P03136;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coat protein VP1 [Contains: Coat protein VP2].
OS Hamster parvovirus H1.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=10799;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83112183; PubMed=6823009;
RA Rhode S.L. III, Paradiso P.R.;
RT "Parvovirus genome: nucleotide sequence of H-1 and mapping of its
RT genes by hybrid-arrested translation.";
RL J. Virol. 45:173-184(1983).
CC -!- SIMILARITY: Belongs to the parvoviruses coat protein family.
CC
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CC -----
DR EMBL; X01457; CAB57285.1; ALT_SEQ.
DR PIR; A03699; VCPVV2.
DR HSSP; P07302; 1WVW.
DR InterPro; IPR001403; Parvo_coat.
DR InterPro; IPR008975; Viral_cap_coat.
DR Pfam; PF00740; Parvo_coat; 1.
KW Coat protein; Glycoprotein.
FT CHAIN 1 722
FT CHAIN 131 722
FT CARBOHYD 178 178
FT CARBOHYD 218 218
FT CARBOHYD 639 639
FT CARBOHYD 639 639

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FT CARBOHYD 647 647 N-linked (GLCNAC. . .) (Potential).
 FT CARBOHYD 675 675 N-linked (GLCNAC. . .) (Potential).
 FT DOMAIN 155 170 Gly-rich.
 SQ SEQUENCE 722 AA; 79737 MW; 688678391AA5DC31 CRC64;
 Query Match 100.0%; Score 54; DB 1; Length 722;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
 Db 156 GGSSGGGGSG 165
 |||||
 |||||

RESULT 6
 Q7XW2 PRELIMINARY; PRT; 893 AA.
 ID Q7XW2
 AC Q7XW2;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE OSJNB0040D15.12 protein.
 GN Names:OSJNB0040D15.12;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID:39947;
 RN [1]
 SEQUENCE FROM N.A.
 RP PubMed:12447439; DOI=10.1038/nature01183;
 RX Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
 Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
 Wang Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
 Liu X., Li T., Li C., Wu Y., Sun T., Lei H., Li T., Guan J.,
 Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
 Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
 Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.,
 Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
 Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y.,
 Han B.;
 RT "Sequence and analysis of rice chromosome 4.";
 RL Nature 420:316-320 (2002).
 DR EMBL; AL606655; CAE04422.2; --
 DR Gramene; Q7XW2; --
 DR GO; GO:0003677; F-DNA binding; IEA.
 DR GO; GO:0006310; P-DNA recombination; IEA.
 DR InterPro; IPR001584; Rve.
 DR InterPro; IPR001878; Znf_CCHC.
 DR Pfam; PF00665; rve; 1.
 DR PRINTS; PR00098; zf-CCHC; 1.
 DR PRINTS; PR00939; C2HCZNFINGER.
 DR SMART; SM00343; Znf_C2HC; 1.
 DR PROSITE; PS00158; ZF_CCHC; 1.
 SQ SEQUENCE 893 AA; 98788 MW; A07AAB99F347B303 CRC64;
 Query Match 100.0%; Score 54; DB 2; Length 893;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
 Db 78 GGSSGGGGSG 87
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 |||||

RESULT 7
 Q9VRU9 PRELIMINARY; PRT; 239 AA.
 ID Q9VRU9
 AC Q9VRU9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CG12330-PA.

GN ORFNames=CG12330;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 SEQUENCE FROM N.A.
 RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RX Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Aht G., Nelson C.R., Baldwin D.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Gabor G.L.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Besley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.B.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 RN [2]
 SEQUENCE FROM N.A.
 RP MEDLINE=22426065; PubMed=12537568;
 RX Celnik S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
 RN [3]
 SEQUENCE FROM N.A.
 RP MEDLINE=22426070; PubMed=12537573;
 RX Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirska R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celnik S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
 RN [4]
 SEQUENCE FROM N.A.
 RP MEDLINE=22426069; PubMed=12537572;
 RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,


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RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnik S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AE003563; AAF0683.1; -.
DR FlyBase; FBgn0035686; CG12330.
DR GO; GO:0042302; F:structural constituent of cuticle; IEA.
DR InterPro; IPR000618; F:structural cuticle.
DR Pfam; PF00379; Chitin bind_4; 1.
DR PRINTS; PR00947; CUTICLE.
DR PROSITE; PS00233; CUTICLE; 1.
SQ SEQUENCE 239 AA; 24412 MW; 98PDP199821EACF9 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 239;
Best Local Similarity 90.0%; Pred. No. 79;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
DB 98 GGSSGGGGGAG 107

RESULT 8
ID Q9L7V8 PRELIMINARY; PRT; 256 AA.
AC Q9L7V8; Q7BY61;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE YscG (hypothetical protein).
GN Name=yscG; OrderedLocNames=HD0589;
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=730;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=35000-HP;
RA Munson R.S. Jr.; Bozue J.A.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=35000HP / ATCC 700724;
RA Munson R.S. Jr.; Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
RT "The complete genome sequence of Haemophilus ducreyi.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF219259; AAF33768.1; -.
DR EMBL; AE017152; AAP95520.1; -.
DR InterPro; IPR007621; DUF477.
DR Pfam; PF04536; DUF477; 1.
DR Complete proteome.
SQ SEQUENCE 256 AA; 28767 MW; F26D6B5B981E56A4 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 256;
Best Local Similarity 90.0%; Pred. No. 85;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
DB 244 GGSSGGGGGAG 253

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnik S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBSJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AE003563; AAF0683.1; -.
DR FlyBase; FBgn0035686; CG12330.
DR GO; GO:0042302; F:structural constituent of cuticle; IEA.
DR InterPro; IPR000618; F:structural cuticle.
DR Pfam; PF00379; Chitin bind_4; 1.
DR PRINTS; PR00947; CUTICLE.
DR PROSITE; PS00233; CUTICLE; 1.
SQ SEQUENCE 239 AA; 24412 MW; 98PDP199821EACF9 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 239;
Best Local Similarity 90.0%; Pred. No. 79;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
DB 98 GGSSGGGGGAG 107

RESULT 8
ID Q9L7V8 PRELIMINARY; PRT; 256 AA.
AC Q9L7V8; Q7BY61;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE YscG (hypothetical protein).
GN Name=yscG; OrderedLocNames=HD0589;
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=730;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=35000-HP;
RA Munson R.S. Jr.; Bozue J.A.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=35000HP / ATCC 700724;
RA Munson R.S. Jr.; Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
RT "The complete genome sequence of Haemophilus ducreyi.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF219259; AAF33768.1; -.
DR EMBL; AE017152; AAP95520.1; -.
DR InterPro; IPR007621; DUF477.
DR Pfam; PF04536; DUF477; 1.
DR Complete proteome.
SQ SEQUENCE 256 AA; 28767 MW; F26D6B5B981E56A4 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 256;
Best Local Similarity 90.0%; Pred. No. 85;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
DB 244 GGSSGGGGGAG 253

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RESULT 9
Q702C2 PRELIMINARY; PRT; 292 AA.
ID Q702C2
AC Q702C2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
DE Hypothetical protein.
OS uncultured crenarchaeote.
OC Archaea; Crenarchaeota; environmental samples.
OX NCBI_TaxID=29281;
RN [1]
RP SEQUENCE FROM N.A.
RA Treusch A.H., Kletzin A., Raddatz G., Ochsenreiter T., Quaiser A.,
RA Meurer G., Schuster S.C., Schleper C.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AJ627421; CAF28702.1; -.
KW Hypothetical protein.
SQ SEQUENCE 292 AA; 31172 MW; ABE908AA4E7DD883 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 292;
Best Local Similarity 90.0%; Pred. No. 96;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
DB 282 GGSSGGGGGAG 291

RESULT 10
Q8F1W0 PRELIMINARY; PRT; 455 AA.
ID Q8F1W0
AC Q8F1W0;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocNames=LA3018;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56501 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AE011484; AAN50216.1; -.
DR InterPro; IPR007621; DUF477.
DR Pfam; PF04536; DUF477; 1.
DR Complete proteome.
SQ SEQUENCE 455 AA; 50518 MW; D3EB4E85920CF847 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 455;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGSSGGGGSG 10
DB 444 GGSSGGGGGAG 453

RESULT 11

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FXD3 MOUSE
ID FXD3 MOUSE STANDARD; PRT; 465 AA.
AC Q61060;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 08-JUN-2004 (Rel. 44, Last annotation update)
DE Forkhead box protein D3 (HNF3/FH transcription factor genesis)
DE (Hepatocyte nuclear factor 3 forkhead homolog 2) (HNF-2).
DE Names:Foxd3; Synonyms=Hfh2;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hromas R.A., Costa R.H., Xu D., Surton J.L.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Labosky P.A., Kaestner K.H.;
RT "The winged helix transcription factor Hfh2 is expressed in neural
RT crest and spinal cord during mouse development.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Probable transcription factor.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Contains 1 fork-head domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U01047; AAA87569.1; -.
DR EMBL; AF067421; AAC28352.1; -.
DR HSSP; Q63245; 2HDC.
DR TRANSFAC; T04166; -.
DR MGD; MG1:1347473; Foxd3.
DR InterPro; IPR001766; TF_Fork_head.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
DR ProDom; PD000425; TF_Fork_head; 1.
DR SMART; SM00339; FH; 1.
DR PROSITE; PS00657; FORK_HEAD_1; 1.
DR PROSITE; PS00658; FORK_HEAD_2; 1.
DR PROSITE; PS00319; FORK_HEAD_3; 1.
KW DNA-binding; Nuclear protein; Transcription regulation.
FT DOMAIN 106 115 Poly-Gly.
FT DNA_BIND 131 225 Fork-head.
FT DOMAIN 252 257 Poly-Ala.
FT DOMAIN 265 270 Poly-Ala.
FT DOMAIN 281 281 Poly-Ala.
FT DOMAIN 380 399 Poly-Gly.
FT DOMAIN 447 457 Poly-Ala.
SQ SEQUENCE 465 AA; 47092 MW; 6F8B5B3D8C7564D CRC64;

Query Match 94.4%; Score 51; DB 1; Length 465;
Best Local Similarity 90.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGSGGGGGSG 10
Db 376 GGSAGGGGGSG 385

RESULT 12
Q8SOK8
ID Q8SOK8 PRELIMINARY; PRT; 559 AA.
AC Q8SOK8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)

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DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE B1078G07.26 protein (P0696G06.3 protein).
GN Name=B1078G07.26; Synonyms=P0696G06.3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartioideae; Oryzoaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Higashita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Sai S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone:P0696G06.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003407; BAB90204.1; -.
DR EMBL; AP003316; BAC06246.1; -.
DR Gramene; Q8SOK8; -.
DR GO; GO:0004500; F:dopamine beta-monoxygenase activity; IEA.
DR GO; GO:0006584; P:catecholamine metabolism; IEA.
DR InterPro; IPR005018; DOMON.
DR InterPro; IPR007649; DUF591.
DR Pfam; PF04569; DUF591; 1.
DR PROSITE; PS50836; DOMON; 1.
SQ SEQUENCE 559 AA; 58234 MW; 90CEBCECEC33883D4 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 559;
Best Local Similarity 90.0%; Pred. No. 1.8e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGSGGGGGSG 10
Db 223 GGTSGGGGGSG 232

RESULT 13
Q7PWR9
ID Q7PWR9 PRELIMINARY; PRT; 582 AA.
AC Q7PWR9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP00000013882 (Fragment).
GN Name=ENSANGP0000001393;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST.
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an

```

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008984; EAA15111.1; --.
FT NON_TER 582
SQ SEQUENCE 582 AA; 64957 MW; 3777CAB9851AB63C CRC64;

Query Match 94.4%; Score 51; DB 2; Length 582;
Best Local Similarity 90.0%; Pred. No. 1.9e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGSSGGGGSG 10
|||:|||||
Db 239 GGSAGGGGSG 248

RESULT 14

Q923A9 PRELIMINARY; PRT; 950 AA.
AC Q923A9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bat2 protein (Fragment).
GN Name=Bat2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zesberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore I., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006564; AAH06564.1; --.
DR MGD; MGI:1915467; Bat2.
DR NON_TER 1
SQ SEQUENCE 950 AA; 99725 MW; E41DE9AB4A6D976 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 950;
Best Local Similarity 90.0%; Pred. No. 3e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGSSGGGGSG 10
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Db 197 GGSAGGGGAG 206

RESULT 15

Q9NHD3

ID Q9NHD3 PRELIMINARY; PRT; 1062 AA.
AC Q9NHD3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Staufen.
GN Name=stau;
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20183617; PubMed=10716936; DOI=10.1093/emboj/19.6.1366;
RA Micklem D.R., Adams J., Grunert S., St Johnston D.;
RT "Distinct roles of two conserved Staufen domains in oskar mRNA
localisation and translation.";
RL EMBO J. 19:1366-1377(2000).
DR HSP; P25159; IEKZ.
DR FlyBase; FBgn0040402; Dvir\stau.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003725; F:double-stranded RNA binding; IEA.
DR InterPro; IPR001159; DS_RBD.
DR Pfam; PF00035; dsrm; 5.
DR SMART; SM00358; DSRM; 5.
DR PROSITE; PS50137; DS_RBD; 5.
SQ SEQUENCE 1062 AA; 112735 MW; D036CC1EC66B41C5 CRC64;

Query Match 94.4%; Score 51; DB 2; Length 1062;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGSSGGGGSG 10
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Db 972 GGAGGGGGSG 981

Search completed: April 8, 2005, 23:36:10
Job time : 180 secs

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